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OM protein - protein search, using sw model

Run on: September 13, 2003, 20:42:19 ; Search time 25 Seconds
(without alignments)
40.855 Million cell updates/sec

Title: US-09-939-293a-19_COPY_56_62
Perfect score: 33
Sequence: 1 AVPIAK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 541936 seqs, 145912426 residues
Total number of hits satisfying chosen parameters: 32153

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*
1: /cgn2_6/ptodata/2/pubppa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubppa/PCT_NEW_PUB.pep.*
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4: /cgn2_6/ptodata/2/pubppa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubppa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubppa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubppa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubppa/US08_PUBCOMB.pep.*
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12: /cgn2_6/ptodata/2/pubppa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubppa/US10A_PUBCOMB.pep.*
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15: /cgn2_6/ptodata/2/pubppa/US10C_PUBCOMB.pep.*
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17: /cgn2_6/ptodata/2/pubppa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubppa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	33	100.0	7	10 US-09-939-293-6	Sequence 6, Appl
2	33	100.0	7	10 US-09-965-967-8	Sequence 8, Appl
3	33	100.0	7	12 US-10-293-371-1	Sequence 1, Appl
4	33	100.0	7	12 US-10-293-371-24	Sequence 24, Appl
5	33	100.0	7	12 US-10-293-371-45	Sequence 45, Appl
6	33	100.0	7	14 US-10-068-569-12	Sequence 12, Appl
7	23	69.7	5	10 US-09-939-293-5	Sequence 5, Appl
8	23	69.7	5	14 US-10-068-569-20	Sequence 20, Appl
9	23	69.7	5	14 US-10-068-569-24	Sequence 24, Appl
10	23	69.7	5	15 US-10-197-634-2	Sequence 2, Appl
11	22	66.7	7	12 US-10-293-371-27	Sequence 27, Appl
12	22	66.7	7	12 US-10-293-371-35	Sequence 35, Appl
13	22	66.7	7	12 US-10-293-371-38	Sequence 38, Appl
14	22	66.7	7	12 US-10-293-371-39	Sequence 39, Appl
15	22	66.7	7	12 US-10-293-371-51	Sequence 51, Appl

	16	20	60.6	7	16	US-10-305-346-8	Sequence 8, Appl
	17	19	57.6	4 <td>10<td>US-09-939-293-13</td><td>Sequence 13, Appl</td></td>	10 <td>US-09-939-293-13</td> <td>Sequence 13, Appl</td>	US-09-939-293-13	Sequence 13, Appl
	18	19	57.6	4 <td>10<td>US-09-965-967-1</td><td>Sequence 1, Appl</td></td>	10 <td>US-09-965-967-1</td> <td>Sequence 1, Appl</td>	US-09-965-967-1	Sequence 1, Appl
	19	19	57.6	4 <td>12<td>US-10-293-371-76</td><td>Sequence 76, Appl</td></td>	12 <td>US-10-293-371-76</td> <td>Sequence 76, Appl</td>	US-10-293-371-76	Sequence 76, Appl
	20	19	57.6	4 <td>14<td>US-10-068-569-21</td><td>Sequence 21, Appl</td></td>	14 <td>US-10-068-569-21</td> <td>Sequence 21, Appl</td>	US-10-068-569-21	Sequence 21, Appl
	21	19	57.6	7 <td>12<td>US-10-293-371-20</td><td>Sequence 20, Appl</td></td>	12 <td>US-10-293-371-20</td> <td>Sequence 20, Appl</td>	US-10-293-371-20	Sequence 20, Appl
	22	18	54.5	6 <td>10<td>US-09-818-656A-20</td><td>Sequence 20, Appl</td></td>	10 <td>US-09-818-656A-20</td> <td>Sequence 20, Appl</td>	US-09-818-656A-20	Sequence 20, Appl
	23	18	54.5	7 <td>9<td>US-09-924-889-5</td><td>Sequence 5, Appl</td></td>	9 <td>US-09-924-889-5</td> <td>Sequence 5, Appl</td>	US-09-924-889-5	Sequence 5, Appl
	24	18	54.5	7 <td>10<td>US-09-884-767A-125</td><td>Sequence 125, App</td></td>	10 <td>US-09-884-767A-125</td> <td>Sequence 125, App</td>	US-09-884-767A-125	Sequence 125, App
	25	18	54.5	7 <td>11<td>US-09-753-139C-4</td><td>Sequence 4, Appl</td></td>	11 <td>US-09-753-139C-4</td> <td>Sequence 4, Appl</td>	US-09-753-139C-4	Sequence 4, Appl
	26	18	54.5	7 <td>11<td>US-09-753-139C-5</td><td>Sequence 5, Appl</td></td>	11 <td>US-09-753-139C-5</td> <td>Sequence 5, Appl</td>	US-09-753-139C-5	Sequence 5, Appl
	27	18	54.5	7 <td>12<td>US-10-293-371-9</td><td>Sequence 9, Appl</td></td>	12 <td>US-10-293-371-9</td> <td>Sequence 9, Appl</td>	US-10-293-371-9	Sequence 9, Appl
	28	18	54.5	7 <td>12<td>US-10-293-371-33</td><td>Sequence 33, Appl</td></td>	12 <td>US-10-293-371-33</td> <td>Sequence 33, Appl</td>	US-10-293-371-33	Sequence 33, Appl
	29	18	54.5	7 <td>12<td>US-10-014-322A-82</td><td>Sequence 82, Appl</td></td>	12 <td>US-10-014-322A-82</td> <td>Sequence 82, Appl</td>	US-10-014-322A-82	Sequence 82, Appl
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	31	17	51.5	5 <td>15<td>US-10-288-966-12</td><td>Sequence 12, Appl</td></td>	15 <td>US-10-288-966-12</td> <td>Sequence 12, Appl</td>	US-10-288-966-12	Sequence 12, Appl
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	33	17	51.5	7 <td>9<td>US-09-096-749A-32</td><td>Sequence 32, Appl</td></td>	9 <td>US-09-096-749A-32</td> <td>Sequence 32, Appl</td>	US-09-096-749A-32	Sequence 32, Appl
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	37	17	51.5	7 <td>12<td>US-10-286-457-108</td><td>Sequence 108, App</td></td>	12 <td>US-10-286-457-108</td> <td>Sequence 108, App</td>	US-10-286-457-108	Sequence 108, App
	38	17	51.5	7 <td>15<td>US-10-174-717A-32</td><td>Sequence 32, Appl</td></td>	15 <td>US-10-174-717A-32</td> <td>Sequence 32, Appl</td>	US-10-174-717A-32	Sequence 32, Appl
	39	17	51.5	7 <td>15<td>US-10-128-966-37</td><td>Sequence 37, Appl</td></td>	15 <td>US-10-128-966-37</td> <td>Sequence 37, Appl</td>	US-10-128-966-37	Sequence 37, Appl
	40	16	48.5	4 <td>10<td>US-09-947-387-46</td><td>Sequence 46, Appl</td></td>	10 <td>US-09-947-387-46</td> <td>Sequence 46, Appl</td>	US-09-947-387-46	Sequence 46, Appl
	41	16	48.5	4 <td>15<td>US-10-100-957A-84</td><td>Sequence 84, Appl</td></td>	15 <td>US-10-100-957A-84</td> <td>Sequence 84, Appl</td>	US-10-100-957A-84	Sequence 84, Appl
	42	16	48.5	5 <td>14<td>US-10-014-485A-123</td><td>Sequence 123, Appl</td></td>	14 <td>US-10-014-485A-123</td> <td>Sequence 123, Appl</td>	US-10-014-485A-123	Sequence 123, Appl
	43	16	48.5	7 <td>10<td>US-09-801-042-12</td><td>Sequence 12, Appl</td></td>	10 <td>US-09-801-042-12</td> <td>Sequence 12, Appl</td>	US-09-801-042-12	Sequence 12, Appl
	44	16	48.5	7 <td>12<td>US-09-777-656A-3</td><td>Sequence 3, Appl</td></td>	12 <td>US-09-777-656A-3</td> <td>Sequence 3, Appl</td>	US-09-777-656A-3	Sequence 3, Appl
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ALIGNMENTS

RESULT 1
US-09-939-293-6
; Sequence 6, Application US/09939293
; Patent No. US20020132786A1
; GENERAL INFORMATION:
; APPLICANT: Alnemerl, Emed S.
; TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE
; FILE REFERENCE: 480140.465
; CURRENT APPLICATION NUMBER: US/09/939,293
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-939-293-6

Query Match 100.0%; Score 33; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.8e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1 AVPIAK 7	I	
Db	1 AVPIAK 7	I	

RESULT 2
US-09-965-967-8
; Sequence 8, Application US/09965967
; Patent No. US2002017757A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Yigong
; TITLE OF INVENTION: Compositions And Methods For Regulating Apoptosis
; FILE REFERENCE: PU-0031 (01-1739-1)
; CURRENT APPLICATION NUMBER: US/09/965,967
; CURRENT FILING DATE: 2001-09-28

;; PRIOR APPLICATION NUMBER: 60/236,574
;; PRIOR FILING DATE: 2000-09-29
;; PRIOR APPLICATION NUMBER: 60/256,830
;; PRIOR FILING DATE: 2000-12-20
;; NUMBER OF SEQ ID NOS: 30
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 8
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-965-967-8

Query Match
Best Local Similarity 100.0%; Score 33; DB 10; Length 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVPIAOK 7
Db 1 AVPIAOK 7

RESULT 3
US-10-293-371-1
;; Sequence 1, Application US/10293371
;; Publication No. US20030157522A1
;; GENERAL INFORMATION:
;; APPLICANT: BOUDREAULT, ALAIN
;; APPLICANT: KORNELOK, ROBERT G.
;; APPLICANT: LACASSE, ERIC
;; APPLICANT: LISTON, PETER
;; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
;; TITLE OF INVENTION: Interaction Screens
;; FILE REFERENCE: 07891/030002
;; CURRENT APPLICATION NUMBER: US/10/293,371
;; PRIOR FILING DATE: 2003-04-08
;; PRIOR APPLICATION NUMBER: US 60/370,934
;; PRIOR FILING DATE: 2002-04-08
;; PRIOR APPLICATION NUMBER: US 60/332,300
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 85
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic
US-10-293-371-1

Query Match
Best Local Similarity 100.0%; Score 33; DB 12; Length 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVPIAOK 7
Db 1 AVPIAOK 7

RESULT 4
US-10-293-371-24
;; Sequence 24, Application US/10293371
;; Publication No. US20030157522A1
;; GENERAL INFORMATION:
;; APPLICANT: BOUDREAULT, ALAIN
;; APPLICANT: KORNELOK, ROBERT G.
;; APPLICANT: LACASSE, ERIC
;; APPLICANT: LISTON, PETER
;; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
;; TITLE OF INVENTION: Interaction Screens
;; FILE REFERENCE: 07891/030002
;; CURRENT APPLICATION NUMBER: US/10/293,371
;; CURRENT FILING DATE: 2003-04-08
;; PRIOR APPLICATION NUMBER: US 60/370,934

;; PRIOR FILING DATE: 2002-04-08
;; PRIOR APPLICATION NUMBER: US 60/332,300
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 85
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 24
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic
US-10-293-371-24

Query Match
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVPIAOK 7
Db 1 AVPIAOK 7

RESULT 5
US-10-293-371-45
;; Sequence 45, Application US/10293371
;; Publication No. US20030157522A1
;; GENERAL INFORMATION:
;; APPLICANT: BOUDREAULT, ALAIN
;; APPLICANT: KORNELOK, ROBERT G.
;; APPLICANT: LACASSE, ERIC
;; APPLICANT: LISTON, PETER
;; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
;; TITLE OF INVENTION: Interaction Screens
;; FILE REFERENCE: 07891/030002
;; CURRENT APPLICATION NUMBER: US/10/293,371
;; PRIOR FILING DATE: 2003-04-08
;; PRIOR APPLICATION NUMBER: US 60/370,934
;; PRIOR FILING DATE: 2002-04-08
;; PRIOR APPLICATION NUMBER: US 60/332,300
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 85
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 45
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic
US-10-293-371-45

Query Match
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Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AVPIAOK 7
Db 1 AVPIAOK 7

RESULT 6
US-10-068-569-12
;; Sequence 12, Application US/10068569
;; Publication No. US20020160975A1
;; GENERAL INFORMATION:
;; APPLICANT: Srinivasula, Srinivasa M.
;; APPLICANT: Fernandes-Alnemri, Teresa
;; APPLICANT: Alnemri, Emdad S.
;; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
;; TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
;; FILE REFERENCE: 480140.475
;; CURRENT APPLICATION NUMBER: US/10/068,569
;; CURRENT FILING DATE: 2002-02-06
;; NUMBER OF SEQ ID NOS: 28

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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-12
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Best Local Similarity 100.0%; Score 33; DB 14; Length 7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AVPIAK 7
Db 1 AVPIAK 7
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RESULT 7
US-09-939-293-5
; Sequence 5, Application US/09939293
; Patent No. US20020132786A1
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; GENERAL INFORMATION:
; APPLICANT: Alnemrl, Emad S.
; TITLE OF INVENTION: AN IAP PEPTIDE OR POLYPEPTIDE
; FILE REFERENCE: 480140.465
; CURRENT APPLICATION NUMBER: US/09/939,293
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-939-293-5
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Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AVPIA 5
Db 1 AVPIA 5
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RESULT 8
US-10-068-569-20
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; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemrl, Teresa
; APPLICANT: Alnemrl, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-20
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Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AVPIA 5
Db 1 AVPIA 5
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RESULT 9
US-10-068-569-24
; Sequence 24, Application US/10068569
; Publication No. US20020160975A1
; GENERAL INFORMATION:
; APPLICANT: Srinivasula, Srinivasa M.
; APPLICANT: Fernandes-Alnemrl, Teresa
; APPLICANT: Alnemrl, Emad S.
; TITLE OF INVENTION: A CONSERVED XIAP-INTERACTION MOTIF IN
; TITLE OF INVENTION: CASPASE-9 AND SMAC/DIABLO FOR MEDIATING APOPTOSIS
; FILE REFERENCE: 480140.475
; CURRENT APPLICATION NUMBER: US/10/068,569
; CURRENT FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-068-569-24
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Query Match
Best Local Similarity 100.0%; Score 23; DB 14; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AVPIA 5
Db 1 AVPIA 5
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RESULT 10
US-10-197-634-2
; Sequence 2, Application US/10197634
; Publication No. US20030073629A1
; GENERAL INFORMATION:
; APPLICANT: Alnemrl, Emad S.
; TITLE OF INVENTION: OMI AND DOMAINS THEREOF THAT DISRUPT
; TITLE OF INVENTION: IAP-CASPASE INTERACTION
; FILE REFERENCE: 480140.479
; CURRENT APPLICATION NUMBER: US/10/197,634
; CURRENT FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-197-634-2
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Query Match
Best Local Similarity 100.0%; Score 23; DB 15; Length 5;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 AVPIA 5
Db 1 AVPIA 5
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RESULT 11
US-10-293-371-27
; Sequence 27, Application US/10293371
; Publication No. US20030157522A1
; GENERAL INFORMATION:
; APPLICANT: BOUDREAULT, ALAIN
; APPLICANT: KORNEJUK, ROBERT G.
; APPLICANT: LACASSE, ERIC
; APPLICANT: LISTON, PETER
; TITLE OF INVENTION: Methods and Reagents for Peptide-B1r
; TITLE OF INVENTION: Interaction Screens
; FILE REFERENCE: 07891/030002
; CURRENT APPLICATION NUMBER: US/10/293,371
; CURRENT FILING DATE: 2003-04-08
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;; PRIOR APPLICATION NUMBER: US 60/370,934
;; PRIOR FILING DATE: 2002-04-08
;; PRIOR APPLICATION NUMBER: US 60/332,300
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 85
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 27
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic
US-10-293-371-27

Query Match
Best Local Similarity 66.7%; Score 22; DB 12; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVPIA 5
1:||||
Db 1 AIPPIA 5

RESULT 12
US-10-293-371-35
;; Sequence 35, Application US/10293371
;; Publication No. US20030157522A1
;; GENERAL INFORMATION:
;; APPLICANT: BOUDREAULT, ALAIN
;; APPLICANT: KORNEILUK, ROBERT G.
;; APPLICANT: LACASSE, ERIC
;; APPLICANT: LISTON, PETER
;; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
;; FILE REFERENCE: 07891/030002
;; CURRENT APPLICATION NUMBER: US/10/293,371
;; CURRENT FILING DATE: 2003-04-08
;; PRIOR APPLICATION NUMBER: US 60/370,934
;; PRIOR FILING DATE: 2002-04-08
;; PRIOR APPLICATION NUMBER: US 60/332,300
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 85
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 35
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic
US-10-293-371-35

Query Match
Best Local Similarity 66.7%; Score 22; DB 12; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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1:||||
Db 1 AIPPIA 5

RESULT 13
US-10-293-371-38
;; Sequence 38, Application US/10293371
;; Publication No. US20030157522A1
;; GENERAL INFORMATION:
;; APPLICANT: BOUDREAULT, ALAIN
;; APPLICANT: KORNEILUK, ROBERT G.
;; APPLICANT: LACASSE, ERIC
;; APPLICANT: LISTON, PETER
;; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
;; FILE REFERENCE: 07891/030002
;; CURRENT APPLICATION NUMBER: US/10/293,371

;; CURRENT FILING DATE: 2003-04-08
;; PRIOR APPLICATION NUMBER: US 60/370,934
;; PRIOR FILING DATE: 2002-04-08
;; PRIOR APPLICATION NUMBER: US 60/332,300
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 85
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 38
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic
US-10-293-371-38

Query Match
Best Local Similarity 66.7%; Score 22; DB 12; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVPIA 5
1:||||
Db 1 AIPPIA 5

RESULT 14
US-10-293-371-39
;; Sequence 39, Application US/10293371
;; Publication No. US20030157522A1
;; GENERAL INFORMATION:
;; APPLICANT: BOUDREAULT, ALAIN
;; APPLICANT: KORNEILUK, ROBERT G.
;; APPLICANT: LACASSE, ERIC
;; APPLICANT: LISTON, PETER
;; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
;; FILE REFERENCE: 07891/030002
;; CURRENT APPLICATION NUMBER: US/10/293,371
;; CURRENT FILING DATE: 2003-04-08
;; PRIOR APPLICATION NUMBER: US 60/370,934
;; PRIOR FILING DATE: 2002-04-08
;; PRIOR APPLICATION NUMBER: US 60/332,300
;; PRIOR FILING DATE: 2001-11-09
;; NUMBER OF SEQ ID NOS: 85
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 39
;; LENGTH: 7
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Synthetic
US-10-293-371-39

Query Match
Best Local Similarity 66.7%; Score 22; DB 12; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVPIA 5
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Db 1 AIPPIA 5

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US-10-293-371-51
;; Sequence 51, Application US/10293371
;; Publication No. US20030157522A1
;; GENERAL INFORMATION:
;; APPLICANT: BOUDREAULT, ALAIN
;; APPLICANT: KORNEILUK, ROBERT G.
;; APPLICANT: LACASSE, ERIC
;; APPLICANT: LISTON, PETER
;; TITLE OF INVENTION: Methods and Reagents for Peptide-Bir
;; FILE REFERENCE: 07891/030002

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; CURRENT APPLICATION NUMBER: US/10/293,371
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/370,934
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/332,300
; PRIOR FILING DATE: 2001-11-09
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-293-371-51
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Query Match          66.7%; Score 22; DB 12; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.8e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY      1 AVPIA 5
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Db       1 AVPIA 5
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Job time : 26 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: September 13, 2003, 20:41:40 ; Search time 80 Seconds
(without alignments)
13.889 Million cell updates/sec

Title: US-09-939-293a-19_COPY_56_62
Perfect score: 33
Sequence: 1 AVPIAOK 7

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 76613

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT.*
- 21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	7	23	ABB76213 Human smac (DIABLO)
2	33	100.0	7	23	AAU78434 Inhibitor of apopt
3	33	100.0	7	23	AAU78487 Smac-7 AV peptide
4	28	84.8	6	23	ABB76214 Human smac (DIABLO)
5	28	84.8	6	23	AAU78486 Smac-6 AV peptide
6	23	69.7	5	23	ABB76215 Human smac (DIABLO)
7	23	69.7	5	23	AAU78433 Inhibitor of apopt
8	23	69.7	5	23	AAU78485 Smac-5 AV peptide
9	23	69.7	5	24	ABF71308 Smac IAP-binding m

10	21	63.6	6	20	AAV14088 Affinity ligand fo
11	21	63.6	7	23	AAU78488 Smac-7R AV peptide
12	20	60.6	7	7	AAPE1490 Angiotensin conver
13	20	60.6	7	14	AAAR30536 ACE inhibiting pep
14	20	60.6	7	15	AAAR37103 Bovine milk beta-c
15	20	60.6	7	24	ABJ37331 G-protein coupled
16	20	60.6	7	24	ABJ37411 G-protein coupled
17	19	57.6	4	23	ABB76220 Human smac (DIABLO)
18	19	57.6	4	23	AAU97413 Human Smac (second
19	19	57.6	4	23	AAU78441 Inhibitor of apopt
20	19	57.6	4	23	AAU78484 Smac-4 AV peptide
21	19	57.6	7	23	ABB98612 Dextrane-saccharas
22	18	54.5	4	23	AAE29600 Metalloprotein C-t
23	18	54.5	4	23	ABG32329 P. vivax circumspo
24	18	54.5	5	12	AAAR12732 Pentapeptide paral
25	18	54.5	5	16	AAAR69964 Pentameric mimotop
26	18	54.5	5	17	AAAR98710 Control peptide fo
27	18	54.5	5	21	AAAR99478 Plant acyltransfer
28	18	54.5	5	21	AAAR52447 Rat GLUT4-eGFP fus
29	18	54.5	6	15	AAAR58328 Hypotensive polype
30	18	54.5	6	21	AAAB12611 Halovar B peptide
31	18	54.5	6	23	AAAR29605 Metalloprotein C-t
32	18	54.5	6	24	ABU13773 Novel human transp
33	18	54.5	7	14	AAAR39444 Crystalline trypti
34	18	54.5	7	15	AAAR58327 Hypotensive polype
35	18	54.5	7	20	AAAR50563 Insulin production
36	18	54.5	7	23	AAAR29595 Metalloprotein #14
37	18	54.5	7	23	AAAR29609 Metalloprotein C-t
38	18	54.5	7	23	AAAR52608 CXC chemokine rece
39	18	54.5	7	23	ABBR3463 Tissue inhibitor o
40	18	54.5	7	23	ABBR3464 Tissue inhibitor o
41	18	54.5	7	23	AAO14001 Cysteine-X-Cystein
42	18	54.5	7	23	AAU81658 Enterokinase recog
43	17	51.5	5	24	ABU64702 Motif-specific and
44	17	51.5	6	21	AAAR35910 Peptide conveying
45	17	51.5	6	22	AAAB9754 Complex sugar boun

ALIGNMENTS

RESULT 1	ABB76213	standard; Peptide; 7 AA.
ID	ABB76213	
XX	ABB76213	
AC	ABB76213	
XX	09-AUG-2002	(first entry)
DT	XX	
XX	Human smac (DIABLO) derived peptide.	
DE	XX	
KW	DIABLO; smac; inhibitor of apoptosis protein; IAP; apoptosis;	
KM	human; cancer; cytostatic; mutant; mutcin.	
XX	XX	
OS	Homo sapiens.	
XX	XX	
FH	Key	Location/Qualifiers
FT	Modified-site	7
FT	/note="optional C-terminal protecting group, e.g. C-terminal amide"	
FT	XX	
PN	WO200230959-A2.	
PD	18-APR-2002.	
XX	XX	
PF	12-OCT-2001; 2001MO-US32121.	
PR	13-OCT-2000; 2000US-0687549.	
XX	XX	
PA	(ABBO) ABBOTT LAB.	
XX	XX	
PI	Fesik SW, Meadows RP, Betz SP, Liu Z, Olejniczak ET, Sun C;	
XX	XX	

DR	WP1; 2002-444169/47.
PT	Novel peptide derived from wild-type human second mitochondria derived
PT	activator of caspase protein useful for identifying candidate
PT	substances to kill cancerous cells -
XX	
PS	Claim 5; Page 7; 26pp; English.
XX	
CC	The present sequence is a peptide derived from wild-type human
CC	second mitochondria derived activator of caspase (smac), also known
CC	as direct inhibitor of apoptosis binding protein with low pI
CC	(DIABLO). The peptide is one of 12 claimed smac (DIABLO)-derived
CC	peptides (see ABB76208-19) which bind to the Bir2 and Bir3 domain
CC	of XIAP, an inhibitor of apoptosis protein (IAP) family member.
CC	Kd values for Bir-3 and Bir-2 are 0.70 +/- 0.09 uM and 9.4 +/- 0.6
CC	uM, respectively, for the present (C-terminally amidated) peptide,
CC	compared with 0.42 +/- 0.02 uM and 2.3 +/- 0.3 uM, respectively,
CC	for full-length smac. Modification of the N-terminal alanine
CC	destroys binding affinity to XIAP, and mutation of the valine,
CC	proline or isoleucine also causes some loss of binding. Amino
CC	acids C-terminal to the isoleucine are not important for binding.
CC	The claimed peptides can be used to identify candidate substances
CC	which induce or promote apoptosis in cells. The assay involves
CC	determination of the ability of candidate compounds to disrupt the
CC	binding interaction between a smac (DIABLO) peptide and an IAP
CC	family member.
XX	
SQ	Sequence 7 AA;
Query Match	100.0%; Score 33; DB 23; Length 7;
Best Local Similarity	100.0%; Pred. No. 9.3e+05;
Matches	7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 AVPIAOK 7
Db	1 AVPIAOK 7
RESULT 2	
AAU78434	
ID	AAU78434 standard; Peptide; 7 AA.
XX	
AC	AAU78434;
XX	
DF	18-JUN-2002 (first entry)
DE	Inhibitor of apoptosis (IAP) protein Smac, mutant Smac-N7.
XX	
KW	Human; Inhibitor of apoptosis; IAP; Smac; Apoptosis; BID; BIR1; BIR2;
XX	Kc12 interacting domain; caspase; BIR domain; BIR3; gene therapy;
KM	neoplastic cell; mutant; tumour.
XX	
OS	Homo sapiens.
OS	Synthetic.
XX	
PN	WO200216418-A2.
PD	28-FEB-2002.
PF	24-AUG-2001; 2001MO-US26492.
PR	24-AUG-2000; 2000US-227735P.
PA	(UYJE-) UNIV JEFFERSON THOMAS.
PI	AInemti ES;
DR	WP1; 2002-304115/34.
PT	Novel Smac peptides and polynucleotides encoding the peptides, useful
PT	for stimulating apoptosis in neoplastic or tumour cell which
PT	overexpresses inhibitor of caspase, and for identifying apoptosis
PT	modulating compounds -

XX		Example 3; Fig 7; 78bp; English.
PS		
CC	The invention relates to an isolated Smac peptide or polypeptide (I)	
CC	and an isolated nucleic acid (II) encoding (I). Also described is a	
XX	method of identifying a compound that inhibits apoptosis, comprising:	
CC	(a) separately contacting several cell populations expressing a	
CC	cytosolic Smac (a Smac isoform that begins with MRSDFE sequence,	
CC	replacing the mitochondrial targeting sequence (residues 1-55 of (I)),	
CC	and residues 56-60 of (I)) and an inhibitor of BID (Bcl2 interacting	
CC	domain) with a compound to be tested for apoptotic inhibiting activity;	
CC	(b) incubating the cell populations with a direct stimulus of the cell	
CC	death pathway; and (c) measuring the specific apoptotic activity of the	
CC	cell populations, where inhibition of the specific apoptotic activity is	
CC	indicative that the compound is an inhibitor of apoptosis. (I) and (II)	
CC	are useful for inducing apoptosis in a cell. The Smac polypeptide and	
CC	polynucleotide are useful for stimulating apoptosis in a neoplastic or	
CC	tumour cell which overexpresses an inhibitor of caspase, where the	
CC	inhibitor inhibits activation or activity of caspase-3, caspase-7 or	
CC	caspase-9. Preferably, the cell overexpresses at least a portion of IAP.	
CC	(I) is useful for identifying an inhibitor or enhancer of a caspase-	
CC	mediated apoptosis which involves contacting a cell transformed or	
CC	transfected with a vector expressing (I) with a candidate inhibitor or	
CC	candidate enhancer; and detecting cell viability, where an increase in	
CC	cell viability indicates the presence of an inhibitor and a decrease in	
CC	cell viability indicates the presence of an enhancer. Optionally, the	
CC	method involves detecting the presence of large and small caspase	
CC	substrates after contacting cell transformed with the vector expressing	
CC	(I), with the candidate compound. A decrease in processing indicates the	
CC	presence of an inhibitor and an increase in the processing indicates the	
CC	presence of an enhancer. Preferably, the large and small substrates of	
CC	caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for	
CC	identifying a compound that inhibits Smac binding to Smac-binding	
CC	molecule (a portion of IAP e.g. a BIR domain such as BIR1, BIR2 or BIR3,	
CC	or a full-length IAP). (II) is useful in gene therapy techniques. The	
CC	present sequence represents the amino acid sequence of Smac mutant	
CC	Smac-N7.	
CC		
XX	Sequence 7 AA;	
SO		
	Query Match 100.0%; Score 33; DB 23; Length 7;	
	Best Local Similarity 100.0%; Pred. No. 9.3e+05;	
	Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 AVPIAQK 7 	
DB	1 AVPIAQK 7	
RESULT 3		
ID	AAU78487 standard; Peptide: 7 AA.	
XX		
AC	AAU78487;	
XX		
DT	18-JUN-2002 (first entry)	
XX		
DE	Smac-7 AV peptide.	
XX		
KW	Apoptosis; Apoptostatic; apoptotic; AV peptide; melanoma; lymphoma;	
OS	Inhibitor of Apoptosis protein; IAP; procaspase-3; tumour cell;	
XX	breast cancer; prostate cancer; lung cancer; pancreatic cancer; smac-7;	
XX	gastric cancer; colon cancer; ovarian cancer; renal cancer; hepatoma;	
KM	sarcoma; smac; second mitochondria-derived activator of caspases.	
XX		
OS	Synthetic.	
XX		
PN	WO200216402-A2.	
PD	28-FEB-2002.	
XX		
FP	23-AUG-2001; 2001MO-US41869.	
XX		

PR 23-AUG-2000; 2000US-0645075.
 XX (TEXA) UNTV TEXAS SYSTEM.
 PA
 XX
 PI Wang X, Du C;
 XX
 DR WPI; 2002-280909/32.
 XX
 PT Composition for enhancing the apoptosis of pathogenic cells,
 PT particularly tumour cells, e.g. breast cancer, prostate cancer, lung
 PT cancer, colon cancer, ovarian cancer or sarcoma, comprises apoptotic
 PT compounds -
 XX
 PS Example 9; Page 28; 40pp; English.
 XX
 CC This invention relates to a method for induction of apoptosis in
 CC pathogenic cells. The method comprises a novel pharmaceutical
 CC composition which comprises an AV peptoid in dosage form and a
 CC pharmaceutical carrier, where the AV peptoid comprises a peptide that
 CC interacts with or inhibits the activity of an inhibitor of Apoptosis
 CC protein (IAP) as measured by IAP binding, procaspase-3 activation or
 CC promotion of apoptosis. The peptoids of the invention are used to
 CC inhibit an inhibitor of Apoptosis protein (IAP). Compositions containing
 CC these peptide are useful for enhancing the apoptosis of pathogenic
 CC cells, particularly tumour cells, e.g. breast cancer, prostate cancer,
 CC lung cancer, pancreatic cancer, gastric cancer, colon cancer, ovarian
 CC cancer, renal cancer, hepatoma, melanoma, lymphoma or sarcoma. The
 CC composition is particularly useful for promoting cell death. The
 CC present sequence represents an AV peptoid (smac-7) used to inhibit
 CC second mitochondria-derived activator of caspases (smac) using the
 CC method of the invention. Smac interacts with and eliminates the activity
 CC of a number of IAP's and as such inhibiting its activity allows the
 CC induction of apoptosis.
 CC
 SQ Sequence 7 AA;
 XX
 XX

Query Match 100.0%; Score 33; DB 23; Length 7;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVPIAQ 7
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 DB 1 AVPIAQ 7

RESULT 4
 ABB76214
 ID ABB76214 standard; Peptide; 6 AA.
 XX
 AC ABB76214;
 XX
 DE 09-AUG-2002 (first entry)
 XX
 DE Human smac (DIABLO) derived peptide.
 XX
 KW DIABLO; smac; inhibitor of apoptosis protein; IAP; apoptosis;
 KW human; cancer; cytostatic; mutant; mutleln.
 XX
 OS Homo sapiens.
 XX
 FT Key Location/Qualifiers
 FT Modified-site 6 /note="Optional C-terminal protecting group,
 FT e.g. C-terminal amide"
 FT
 XX
 PN WO200230959-A2.
 XX
 PD 18-APR-2002.
 XX
 PF 12-OCT-2001; 2001WO-US32121.
 XX
 PR 13-OCT-2000; 2000US-0687549.
 XX

PA (ABBO) ABBOTT LAB.
 XX
 XX Resik SW, Meadows RP, Betz SP, Liu Z, Olejniczak ET, Sun C;
 XX
 DR WPI; 2002-444169/47.
 XX
 PT Novel peptide derived from wild-type human second mitochondria derived
 PT activator of caspase protein useful for identifying candidate
 PT substances to kill cancerous cells -
 XX
 PS Claim 5; Page 7; 26pp; English.
 XX
 CC The present sequence is a peptide derived from wild-type human
 CC second mitochondria derived activator of caspase (smac), also known
 CC as direct inhibitor of apoptosis binding protein with low PI
 CC (DIABLO). The peptide is one of 12 claimed smac (DIABLO)-derived
 CC peptides (see ABB76208-19) which bind to the Bir2 and Bir3 domain
 CC of XIAP, an inhibitor of apoptosis protein (IAP) family member.
 CC Kd values for Bir-3 and Bir-2 are 0.80 +/- 0.2 uM and 8.9 +/- 0.6
 CC uM, respectively, for the present (C-terminally amidated) peptide,
 CC compared with 0.42 +/- 0.02 uM and 2.3 +/- 0.3 uM, respectively,
 CC for full-length smac. Modification of the N-terminal alanine
 CC destroys binding affinity to XIAP, and mutation of the valine,
 CC proline or isoleucine also causes some loss of binding. Amino
 CC acids C-terminal to the isoleucine are not important for binding.
 CC The claimed peptides can be used to identify candidate substances
 CC which induce or promote apoptosis in cells. The assay involves
 CC determination of the ability of candidate compounds to disrupt the
 CC binding interaction between a smac (DIABLO) peptide and an IAP
 CC family member.
 CC
 SQ Sequence 6 AA;
 XX
 XX

Query Match 84.8%; Score 28; DB 23; Length 6;
 Best Local Similarity 100.0%; Pred. No. 9.3e+05;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVPIAQ 6
 |||||
 DB 1 AVPIAQ 6

RESULT 5
 AAU78486
 ID AAU78486 standard; Peptide; 6 AA.
 XX
 AC AAU78486;
 XX
 DE 18-JUN-2002 (first entry)
 XX
 DE Smac-6 AV peptoid.
 XX
 KW Apoptosis; cytostatic; apoptotic; AV peptoid; melanoma; lymphoma;
 KW inhibitor of Apoptosis protein; IAP; procaspase-3; tumour cell;
 KW breast cancer; prostate cancer; lung cancer; pancreatic cancer; smac-6;
 KW gastric cancer; colon cancer; ovarian cancer; renal cancer; hepatoma;
 KW sarcoma; smac; second mitochondria-derived activator of caspases.
 XX
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT Modified-site 28 WO200216402-A2.
 FT
 XX
 PD 28-FEB-2002.
 XX
 PF 23-AUG-2001; 2001WO-US41869.
 XX
 PR 23-AUG-2000; 2000US-0645075.
 XX
 PA (TEXA) UNTV TEXAS SYSTEM.
 XX
 PI Wang X, Du C;
 XX
 DR WPI; 2002-280909/32.

XX Composition for enhancing the apoptosis of pathogenic cells,
PT particularly tumour cells, e.g. breast cancer, prostate cancer, lung
PT cancer, colon cancer, ovarian cancer or sarcoma, comprises apoptotic
PT compounds -
PS
XX Example 9; Page 28; 40pp; English.
XX
CC This invention relates to a method for induction of apoptosis in
CC pathogenic cells. The method comprises a novel pharmaceutical
CC composition which comprises an AV peptide in dosage form and a
CC pharmaceutical carrier, where the AV peptide comprises a peptide that
CC interacts with or inhibits the activity of an inhibitor of Apoptosis
CC protein (IAP) as measured by IAP binding, procaspase-3 activation or
CC promotion of apoptosis. The peptides of the invention are used to
CC inhibit an inhibitor of Apoptosis protein (IAP). Compositions containing
CC these peptides are useful for enhancing the apoptosis of pathogenic
CC cells, particularly tumour cells, e.g. breast cancer, prostate cancer,
CC lung cancer, pancreatic cancer, gastric cancer, colon cancer, ovarian
CC cancer, renal cancer, hepatoma, melanoma, lymphoma or sarcoma. The
CC composition is particularly useful for promoting cell death. The
CC present sequence represents an AV peptide (smac-6) used to inhibit
CC second mitochondria-derived activator of caspases (smac) using the
CC method of the invention. Smac interacts with and eliminates the activity
CC of a number of IAP's and as such inhibiting its activity allows the
CC induction of apoptosis.
CC
XX
SQ Sequence 6 AA;
Query Match 84.8%; Score 28; DB 23; Length 6;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVPIAQ 6
Db 1 AVPIAQ 6
|||||
|
RESULT 6
ABR76215
ID ABR76215 standard; Peptide; 5 AA.
XX
AC ABR76215;
XX
DT 09-AUG-2002 (first entry)
XX
DE Human smac (DIABLO) derived peptide.
XX
KW DIABLO; smac; inhibitor of apoptosis protein; IAP; apoptosis;
KW human; cancer; cytostatic; mutant; mutain.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 5 /note="optional C-terminal protecting group,
FT e.g. C-terminal amide"
XX
XX WO200230959-A2.
XX
XX 18-APR-2002.
XX
XX 12-OCT-2001; 2001WO-US32121.
XX
XX 13-OCT-2000; 2000US-0687549.
XX
XX (ABB0) ABBOTT LAB.
XX
XX Fesik SW, Meadows RP, Betz SP, Liu Z, Olejniczak ET, Sun C;
XX
XX WPI; 2002-444169/47.
XX
PT Novel peptide derived from wild-type human second mitochondria derived

PT activator of caspase protein useful for identifying candidate
PT substances to kill cancerous cells -
PS
XX Claim 5; Page 7; 26pp; English.
XX
CC The present sequence is a peptide derived from wild-type human
CC second mitochondria derived activator of caspase (smac), also known
CC as direct inhibitor of apoptosis binding protein with low pI
CC (DIABLO). The peptide is one of 12 claimed smac (DIABLO)-derived
CC peptides (see ABR76208-19) which bind to the Bir2 and Bir3 domain
CC of XIAP, an inhibitor of apoptosis protein (IAP) family member.
CC Kd values for Bir-3 and Bir-2 are 0.64 +/- 0.07 uM and 5.5 +/- 0.5
CC uM, respectively, for the present (C-terminally amidated) peptide,
CC compared with 0.42 +/- 0.02 uM and 2.3 +/- 0.3 uM, respectively,
CC for full-length smac, showing that a peptide of 5 amino acids
CC retained full binding affinity to the Bir3 domain of XIAP.
CC Modification of the N-terminal alanine destroyed binding affinity
CC to XIAP, and mutation of the valine, proline or isoleucine also
CC caused some loss of binding. The claimed peptides can be used to
CC identify candidate substances which induce or promote apoptosis in
CC cells. The assay involves determination of the ability of
CC candidate compounds to disrupt the binding interaction between a
CC smac (DIABLO) peptide and an IAP family member.
CC
XX
SQ Sequence 5 AA;
Query Match 69.7%; Score 23; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVPIA 5
Db 1 AVPIA 5
|||||
|
RESULT 7
AAU78433
ID AAU78433 standard; Peptide; 5 AA.
XX
AC AAU78433;
XX
DT 18-JUN-2002 (first entry)
XX
DE Inhibitor of apoptosis (IAP) protein Smac, long isoform peptide.
XX
KW Human; inhibitor of apoptosis; IAP; Smac; apoptosis; BID; BIR1; BIR2;
KW Bcl2 interacting domain; caspase; BIR domain; BIR3; gene therapy;
KW neoplastic cell; tumour.
XX
OS Homo sapiens.
XX
XX WO200216418-A2.
XX
XX 28-FEB-2002.
XX
XX 24-AUG-2001; 2001WO-US26492.
XX
XX 24-AUG-2000; 2000US-227735P.
XX
XX (UYJE-) UNIV JEFFERSON THOMAS.
XX
XX Alnemrl ES;
XX
XX WPI; 2002-304115/34.
XX
XX
XX Novel Smac peptides and polynucleotides encoding the peptides, useful
XX for stimulating apoptosis in neoplastic or tumour cell which
XX overexpresses inhibitor of caspase, and for identifying apoptosis
XX modulating compounds -
XX
XX Example 5; Fig 12; 78pp; English.
XX
XX The invention relates to an isolated Smac peptide or polypeptide (I)

CC and an isolated nucleic acid (II) encoding (I). Also described is a
CC method of identifying a compound that inhibits apoptosis, comprising:
CC (a) separately contacting several cell populations expressing a
CC cytosolic Smac (a Smac isoform that begins with MKSPFY sequence,
CC replacing the mitochondrial targeting sequence (residues 1-55 of (I)),
CC and residues 56-60 of (I)) and an inhibitor of BID (Bcl2 interacting
CC domain) with a compound to be tested for apoptotic inhibiting activity;
CC (b) incubating the cell populations with a direct stimulus of the cell
CC death pathway; and (c) measuring the specific apoptotic activity of the
CC cell populations, where inhibition of the specific apoptotic activity is
CC indicative that the compound is an inhibitor of apoptosis. (I) and (II)
CC are useful for inducing apoptosis in a cell. The Smac polypeptide and
CC polynucleotide are useful for stimulating apoptosis in a neoplastic or
CC tumour cell which overexpresses an inhibitor of caspase-3, caspase-7 or
CC inhibitor inhibits activation or activity of caspase-3, caspase-7 or
CC caspase-9. Preferably, the cell overexpresses at least a portion of IAP.
CC (I) is useful for identifying an inhibitor or enhancer of a caspase-
CC mediated apoptosis which involves contacting a cell transformed or
CC transfected with a vector expressing (I) with a candidate inhibitor or
CC candidate enhancer; and detecting cell viability, where an increase in
CC cell viability indicates the presence of an inhibitor and a decrease in
CC cell viability indicates the presence of an enhancer. Optionally, the
CC method involves detecting the presence of large and small caspase
CC subunits after contacting cell transformed with the vector expressing
CC (I), with the candidate compound. A decrease in processing indicates the
CC presence of an inhibitor and an increase in the processing indicates the
CC presence of an enhancer. Preferably, the large and small subunits of
CC caspase-3, caspase-7 or caspase-9 are detected. (I) is also useful for
CC identifying a compound that inhibits Smac binding to Smac-binding
CC molecule (a portion of IAP e.g. a BIR domain such as BIR1, BIR2 or BIR3,
CC or a full-length IAP). (II) is useful in gene therapy techniques. The
CC present sequence represents the amino acid sequence of Smac protein long
CC isoform peptide.
CC
CC
SQ Sequence 5 AA:

Query Match 69.7%; Score 23; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVPIA 5
|||||
Db 1 AVPIA 5

RESULT 8
AAU78485
ID AAU78485 standard; peptide; 5 AA.
AC AAU78485;
XX
XX
DT 18-JUN-2002 (first entry)
XX
XX
DE Smac-5 AV peptide.
XX
XX
KM Apoptosis: cytosolic; apoptotic; AV peptide; melanoma; lymphoma;
KM inhibitor of Apoptosis protein; IAP; procaspase-3; tumour cell;
KM breast cancer; prostate cancer; lung cancer; pancreatic cancer; smac-5;
KM gastric cancer; colon cancer; ovarian cancer; renal cancer; hepatoma;
KM sarcoma; smac; second mitochondria-derived activator of caspases.
XX
OS Synthetic.
XX
PN WO200216402-A2.
XX
PD 28-FEB-2002.
XX
PF 23-AUG-2001; 2001WO-US41869.
XX
PR 23-AUG-2000; 2000US-0645075.
XX
PA (TEXA) UNIV TEXAS SYSTEM.
XX

PI Wang X, Du C;
XX
DR WPI; 2002-280909/32.
XX
PT Composition for enhancing the apoptosis of pathogenic cells,
PT particularly tumour cells, e.g. breast cancer, prostate cancer, lung
PT cancer, colon cancer, ovarian cancer or sarcoma, comprises apoptotic
PT compounds -
XX
PS Example 9; Page 28; 40pp; English.
XX
XX This invention relates to a method for induction of apoptosis in
CC pathogenic cells. The method comprises a novel pharmaceutical
CC composition which comprises an AV peptide in dosage form and a
CC pharmaceutical carrier, where the AV peptide comprises a peptide that
CC interacts with or inhibits the activity of an inhibitor of Apoptosis
CC protein (IAP) as measured by IAP binding, procaspase-3 activation or
CC promotion of apoptosis. The peptides of the invention are used to
CC inhibit an inhibitor of Apoptosis protein (IAP). Compositions containing
CC these peptides are useful for enhancing the apoptosis of pathogenic
CC cells, particularly tumour cells, e.g. breast cancer, prostate cancer,
CC lung cancer, pancreatic cancer, gastric cancer, colon cancer, ovarian
CC cancer, renal cancer, hepatoma, melanoma, lymphoma or sarcoma. The
CC composition is particularly useful for promoting cell death. The
CC present sequence represents an AV peptide (smac-5) used to inhibit
CC second mitochondria-derived activator of caspases (smac) using the
CC method of the invention. Smac interacts with and eliminates the activity
CC of a number of IAP's and as such inhibiting its activity allows the
CC induction of apoptosis.
CC
CC
SQ Sequence 5 AA:

Query Match 69.7%; Score 23; DB 23; Length 5;
Best Local Similarity 100.0%; Pred. No. 9.3e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVPIA 5
|||||
Db 1 AVPIA 5

RESULT 9
ABP71308
ID ABP71308 standard; peptide; 5 AA.
AC ABP71308;
XX
XX
DT 28-APR-2003 (first entry)
XX
XX
DE Smac IAP-binding motif peptide.
XX
XX
KM Oml; Htra2; serine protease; inhibitor of apoptosis protein; IAP;
KM caspase; apoptosis; cytosolic; immunosuppressive; neuroprotective;
KM vasotropic; gene therapy; human.
XX
XX
OS Homo sapiens.
XX
PN WO2003006680-A2.
XX
PD 23-JAN-2003.
XX
PF 15-JUL-2002; 2002WO-US22658.
XX
PR 13-JUL-2001; 2001US-305378P.
PR 14-DEC-2001; 2001US-340163P.
XX
PA (UYJE-) UNIV JEFFERSON THOMAS.
XX
PI Alnemri ES;
XX
DR WPI; 2003-221760/21.
XX
PT New Oml nucleic acids and peptides that bind to an inhibitor of

CC lung cancer, pancreatic cancer, gastric cancer, colon cancer, ovarian
CC cancer, renal cancer, hepatoma, melanoma, lymphoma or sarcoma. The
CC composition is particularly useful for promoting cell death. The
CC present sequence represents an AV peptide (smac-7R) used to inhibit
CC second mitochondria-derived activator of caspases (smac) using the
CC method of the invention. Smac interacts with and eliminates the activity
CC of a number of IAP's and as such inhibiting its activity allows the
CC induction of apoptosis.
XX
SQ Sequence 7 AA;
Query Match 63.6%; Score 21; DB 23; Length 7;
Best Local Similarity 60.0%; Pred. No. 9.3e+05;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 AVPIA 5
|:|:|
Db 3 AVPPA 7
RESULT 12
AAP61490
ID AAP61490 standard; peptide; 7 AA.
XX
AC AAP61490;
XX
DT 25-MAR-2003 (updated)
DT 10-MAR-2003 (updated)
DT 18-JUL-1991 (first entry)
XX
DE Angiotensin converting enzyme inhibitor.
XX
KM hypotensive peptide.
XX
OS Bos taurus.
OS Synthetic.
XX
PN JPE1036226-A.
XX
PD 20-FEB-1986.
XX
PF 28-JUL-1984; 84JP-0158324.
XX
PR 28-JUL-1984; 84JP-0158324.
XX
PA (AGEN) AGENCY OF IND SCI & TECHNOLOGY.
XX
DR WPI; 1986-090774/14.
XX
PT New angiotensin converting enzyme inhibitor - having hypotensive
PT activity with low side effects.
XX
PS Claim 1; Page 187; 4pp; Japanese.
XX
CC Inhibitor has hypotensive activity with minimal side effects, it may
CC be simply prepared from bovine caesin.
CC (Updated on 10-MAR-2003 to add missing OS field.)
CC (Updated on 25-MAR-2003 to correct PA field.)
XX
SQ Sequence 7 AA;
Query Match 60.6%; Score 20; DB 7; Length 7;
Best Local Similarity 57.1%; Pred. No. 9.3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 AVPIAOK 7
|:|:|:
Db 1 AVPPOR 7
RESULT 13
AAR30536
ID AAR30536 standard; peptide; 7 AA.

XX
XX AAR30536;
AC
XX 07-MAY-1993 (first entry)
DT
XX
XX ACE inhibiting peptide #3.
DE
XX
XX angiotensin converting enzyme inhibitor; vasodpressor activity;
KW low blood pressure; high blood pressure; hypertension; hypotension;
KW hypertensive; hypotensive.
XX
OS Synthetic.
XX
PN JP04341193-A.
XX
PD 27-NOV-1992.
XX
PF 14-MAY-1991; 91JP-0139772.
XX
PR 14-MAY-1991; 91JP-0139772.
XX
PR 14-MAY-1991; 91JP-0139772.
XX
PA (KANE) KANEBO LTD.
XX
DR WPI; 1993-013419/02.
XX
XX Prodn. of angiotensin converting enzyme inhibiting peptide - by
PT sepy. and purifying enzyme decomposition prod. of casein using
PT ion exchange and hydrophobic resins
XX
PS Claim 1; Page 1; 7pp; Japanese.
XX
XX This angiotensin converting enzyme (ACE) inhibitor is derived by a
CC novel method of Prodn. This comprises separation of an enzyme digest
CC of casein (milk-derived) and purification by ion exchange resin and
CC hydrophobic resin.
XX
SQ Sequence 7 AA;
Query Match 60.6%; Score 20; DB 14; Length 7;
Best Local Similarity 57.1%; Pred. No. 9.3e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 AVPIAOK 7
|:|:|:
Db 1 AVPPOR 7
RESULT 14
AAR37103
ID AAR37103 standard; peptide; 7 AA.
XX
AC AAR37103;
XX
XX 21-MAY-1995 (first entry)
DT
XX
DE Bovine milk beta-casein enzymatic fragment.
XX
XX Beta-casein; enzymatic hydrolysate; cosmetics; skin disorders;
KW wrinkles.
XX
OS Bos Taurus.
XX
PN JP06166615-A.
XX
PD 14-JUN-1994.
XX
PF 01-DEC-1992; 92JP-0321624.
XX
PR 01-DEC-1992; 92JP-0321624.
XX
PA (POK) POLA CHEM IND INC.
XX
DR WPI; 1994-230615/28.

XX Cosmetics for treating skin disorders and wrinkles - containing
 PT enzymatic hydrolysate of human or bovine milk beta-casein
 XX
 PS Claim 2; Page 2; 7pp; Japanese.
 XX
 CC The invention relates to cosmetics containing human or bovine milk
 CC beta-casein enzymatic hydrolysate. The cosmetics are used for
 CC improving skin disorders and/or wrinkles. They are more effective
 CC than previously used polysaccharides, sugar alcohols, glycerol,
 CC glycols, etc.
 CC The present sequence is one component of the bovine milk beta-casein
 CC enzymatic hydrolysate.
 CC
 SQ Sequence 7 AA;
 Query Match 60.6%; Score 20; DB 15; Length 7;
 Best Local Similarity 57.1%; Pred. No. 9.3e+05;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVPIAQK 7
 ||| |
 |:
 Db 1 AVYPPQR 7

SQ Sequence 7 AA;
 Query Match 60.6%; Score 20; DB 24; Length 7;
 Best Local Similarity 66.7%; Pred. No. 9.3e+05;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 VPIAQK 7
 || ||
 || ||
 Db 2 VPIQK 7

Search completed: September 13, 2003, 20:43:39
 Job time : 81 secs

RESULT 15
 AB037331
 ID AB037331 standard; Peptide; 7 AA.
 XX
 AC AB037331;
 XX
 DT 08-MAY-2003 (first entry)
 XX
 DE G-protein coupled receptor peptide region #43.
 XX
 KM Compound library; microenvironment; G-protein Coupled Receptor; GPCR.
 XX
 OS Unidentified.
 XX
 PN W02003004147-A2.
 XX
 PD 16-JAN-2003.
 XX
 PF 05-JUL-2002; 2002WO-GB03094.
 XX
 PR 06-JUL-2001; 2001GB-0016570.
 XX
 PA (BIOF-) BIOFOCUS PLC.
 XX
 PI Crossley R, Rose VS, Stevens AP;
 XX
 DR WPI; 2003-221549/21.
 XX
 PT Producing compound library, by generating biological target model using
 PT target sequence information, defining microenvironments interacting
 PT with ligand and motifs interacting with microenvironment, and
 PT assembling motifs -
 XX
 PS Disclosure; Fig 3; 39pp; English.
 XX
 CC The invention relates to a novel method for producing a compound library.
 CC The novel method involves reducing a biological target into a group of
 CC one or more amino acids required for interaction with a ligand, to
 CC generate a model of the biological target, using the model to define a
 CC microenvironment in the biological target capable of interacting with the
 CC ligand, defining motifs which interact with the microenvironment, and
 CC assembling the motifs to generate a compound library for synthesis. The
 CC novel method is useful to produce compound libraries for screening
 CC natural ligands such as peptides and proteins or for producing chemical
 CC compounds based on drug motifs for screening. This sequence represents a
 CC peptide of a G-protein Coupled Receptor (GPCR), which relates to the
 CC novel compound library production method of the invention.
 CC
 XX

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OM protein - protein search, using sw model

Run on: September 13, 2003, 20:41:40 ; Search time 38 seconds
(without alignments)
17.715 Million cell updates/sec

Title: US-09-939-293a-19_COPY_56_62

Perfect score: 33
Sequence: 1 AVPIAK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 456

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14	42.4	5	2	E60274
2	13	39.4	5	2	JN0860
3	13	39.4	6	2	A61140
4	13	39.4	7	2	ECMOCR
5	12	36.4	5	2	A60521
6	12	36.4	5	2	S11127
7	12	36.4	6	2	A37765
8	12	36.4	7	2	S66442
9	11	33.3	4	2	I54357
10	11	33.3	5	2	B22565
11	11	33.3	5	2	B37988
12	11	33.3	5	2	US0319
13	11	33.3	6	2	A61049
14	11	33.3	6	2	PO0008
15	11	33.3	6	2	B60110
16	11	33.3	6	2	I65546
17	11	33.3	7	2	B61491
18	11	33.3	7	2	PM0150
19	11	33.3	7	2	S42620
20	11	33.3	7	2	A39690
21	10	30.3	3	3	E37196
22	10	30.3	3	3	F37196
23	10	30.3	4	2	E44823
24	10	30.3	5	2	JN0862
25	10	30.3	5	2	PO0009
26	10	30.3	5	2	G37196
27	10	30.3	7	2	A61081
28	10	30.3	7	2	PS0254
29	10	30.3	7	2	I46868

30	9	27.3	4	2	A32039	tyrosine-melanocyte
31	9	27.3	4	2	PT0534	T-cell receptor be
32	9	27.3	5	2	PT0659	T-cell receptor be
33	9	27.3	6	2	A44916	mosquitocidal toxin
34	9	27.3	6	2	PC4127	hypothetical 6 pro
35	9	27.3	6	4	A35039	hypothetical colla
36	9	27.3	6	4	S15596	ori 3 rara 5'-regl
37	9	27.3	7	2	S19630	ribosomal protein
38	9	27.3	7	2	PO0727	H2 class I protein
39	9	27.3	7	2	S71299	ICL2 protein - Par
40	9	27.3	7	2	A28340	myomodulin - Calli
41	9	27.3	7	2	S09027	carboxylesterase (
42	9	27.3	7	2	PT0269	Ig heavy chain CRD
43	9	27.3	7	2	I48105	dihydrofolate redu
44	9	27.3	7	2	I48086	DNA topoisomerase
45	9	27.3	7	2	PH0932	T-cell receptor be

ALIGNMENTS

RESULT 1
E60274
major protein antigen MP763 - Mycobacterium tuberculosis (fragment)
C/Species: Mycobacterium tuberculosis
C/Date: 11-Dec-1992 #sequence_rev1510n 11-Dec-1992 #text_change 30-Sep-1993
R/Nagel, S.; Miker, H.G.; Harboe, M.; Kinomoto, M.
Infect. Immun. 59, 372-382, 1991
A/Title: Isolation and partial characterization of major protein antigens in the cult
A/Reference number: A60274; MUID:9109989; PMID:1898899
A/Accession: E60274
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-5 <NAC>

Query Match 42.4% Score 14; DB 2; Length 5;
Best Local Similarity 75.0% Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVPI 4
DB 1 AVPI 4
RESULT 2
JN0860
peptidyl-dipeptidase A inhibitory peptide C107 - striped bonito
C/Species: Sarda orientalis (striped bonito)
C/Date: 10-Mar-1994 #sequence_rev1510n 10-Mar-1994 #text_change 07-May-1999
R/Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.
Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993
A/Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory
A/Reference number: JN0860; MUID:9408036; PMID:7764272
A/Accession: JN0860
A/Molecule type: protein
A/Residues: 1-5 <MAT>
A/Experimental source: intestine
C/Comment: The carboxyl-terminus is essential for the protein's expression of angioten
C/Superfamily: bradykinin-potentiating peptide
C/Keywords: angiotensin-converting enzyme inhibitor

Query Match 39.4% Score 13; DB 2; Length 5;
Best Local Similarity 60.0% Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVPIA 5
DB 1 ALPHA 5

RESULT 3

A61140
Sperm acrosomal protein - spoonworm (Urechis caupo) (fragment)
C:Species: Urechis caupo
C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-Apr-1994
C:Accession: A61140
R:Gould, M.C.; Stephanou, J.L.
Dev. Biol. 146, 508-518, 1991
A:Title: Peptides from sperm acrosomal protein that initiate egg development.
A:Reference number: A61140; MUID:91323672; PMID:1864468
A:Accession: A61140
A:Molecule type: protein
A:Residues: 1-6 <GOU>

Query Match 39.4%; Score 13; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 IAKK 7
Db 1 VAKK 4

RESULT 4
ECMUCR
catch-relaxing peptide - blue mussel
N:Alternate names: GARP
C:Species: Mytilus edulis (blue mussel)
C:Date: 20-Jun-2000 #sequence_revision 20-Jun-2000 #text_change 20-Jun-2000
C:Accession: A29342
R:Hirata, T.; Kubota, I.; Takahatake, I.; Kawahara, A.; Shimamoto, N.; Muneoka, Y.
Brain Res. 422, 374-376, 1987
A:Title: Catch-relaxing peptide isolated from Mytilus pedal ganglia.
A:Reference number: A29342; MUID:88052022; PMID:3676797
A:Accession: A29342
A:Molecule type: protein
A:Residues: 1-7 <HIR>
C:Comment: This peptide exhibits both potentiating (contraction) and inhibitory (relaxat
C:Superfamily: unassigned animal peptides
C:Keywords: amidated carboxyl end; hormone; retractor muscle
F:7/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match 39.4%; Score 13; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVPI 4
Db 1 AMPM 4

RESULT 5
A60521
glycogen phosphorylase (PG 2.4.1.1), muscle - mullet (Liza ramada) (fragment)
N:Alternate names: glycogen phosphorylase b
C:Species: Liza ramada
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 11-May-2000
C:Accession: A60521
R:Bonomusa, L.; Baanante, I.V.
Comp. Biochem. Physiol. B 95, 295-301, 1990
A:Title: Purification and characterization of glycogen phosphorylase B from skeletal mus
A:Reference number: A60521; MUID:90227907; PMID:2109669
A:Accession: A60521
A:Molecule type: protein
A:Residues: 1-5 <BON>
C:Superfamily: phosphorylase
C:Keywords: glycosyltransferase; hexosyltransferase; phosphoprotein
F:3/Binding site: phosphate (Ser) (covalent) (by phosphorylase b kinase) #status experim

Query Match 36.4%; Score 12; DB 2; Length 5;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVP 3

Db 3 SVP 5

RESULT 6
S1127
phosphoprotein, bone - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 04-Mar-2000
C:Accession: S1127; S1128
R:Mikuni-Takagaki, Y.; Glimcher, M.J.
Biochem. J. 268, 585-591, 1990
A:Title: Post-translational processing of chicken bone phosphoproteins. Identificatio
A:Reference number: S1127; MUID:90303246; PMID:2363696
A:Accession: S1127
A:Molecule type: protein
A:Status: preliminary
A:Residues: 1-5 <MIK1>
A:Accession: S1128
A:Status: preliminary
A:Molecule type: protein
A:Residues: 'X', 2-5 <MIK2>
C:Keywords: phosphoprotein

Query Match 36.4%; Score 12; DB 2; Length 5;
Best Local Similarity 25.0%; Pred. No. 2.8e+05;
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 PIAQ 6
Db 2 PVSK 5

RESULT 7
A3765
hypothetical protein (csma 5' region) - Chloroflexus aurantiacus (fragment)
C:Species: Chloroflexus aurantiacus
C:Date: 31-May-1991 #sequence_revision 31-May-1991 #text_change 30-Sep-1993
C:Accession: A37765
R:Theroux, S.J.; Redlinger, T.E.; Fuller, R.C.; Robinson, S.J.
J. Bacteriol. 172, 4497-4504, 1990
A:Title: Gene encoding the 5.7-kilodalton chlorosome protein of Chloroflexus aurantia
A:Reference number: A37765; MUID:90330558; PMID:2376566
A:Accession: A37765
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-6 <THE>
A:Cross-references: GB:M33964

Query Match 36.4%; Score 12; DB 2; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 IAKK 7
Db 3 MAQR 6

RESULT 8
S66442
glutathione S-transferase P - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S66442
R:Nishihira, J.; Sakai, M.; Nishi, S.; Hatanaka, Y.
Eur. J. Biochem. 232, 106-110, 1995
A:Title: Identification of the electrophilic substrate-binding site of glutathione S-
A:Reference number: S66442; MUID:96046035; PMID:7556138
A:Accession: S66442
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <NIS>

Query Match 36.4%; Score 12; DB 2; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVP 3
 II
 Db 1 ALP 3

RESULT 9

154357
 schwannomin - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
 C:Accession: 154357
 R:Hyunh, D.P.; Nechiporuk, T.; Pulst, S.
 Hum. Mol. Genet. 3, 1075-1079, 1994
 A:Title: Alternative transcripts in the mouse neurofibromatosis type 2 (NF2) gene are co
 A:Reference number: 154357; MUID:95072570; PMID:7381675
 C:Accession: 154357
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-4 <RES>
 A:Cross-references: GB:U28838; NID:9454836; PIDN:AAA57150.1; PID:9601923
 C:Genetics:
 A:Gene: NF2

Query Match 33.3%; Score 11; DB 2; Length 4;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VP 3
 II
 Db 1 VP 2

RESULT 10

B22565
 R-phycoerythrin alpha-2 chain - red alga (Gastrocionium coulteri) (fragment)
 C:Species: Gastrocionium coulteri
 C:Date: 07-Mar-1988 #sequence_revision 07-Mar-1988 #text_change 23-Mar-1993
 C:Accession: B22565
 R:Klotz, A.V.; Glazer, A.N.
 J. Biol. Chem. 260, 4856-4863, 1985
 A:Title: Characterization of the bilin attachment sites in R-phycoerythrin.
 A:Reference number: A22565; MUID:85182601; PMID:3886644
 A:Accession: B22565
 A:Molecule type: protein
 A:Residues: 1-5 <KID>

Query Match 33.3%; Score 11; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VP 3
 II
 Db 3 VP 4

RESULT 11

B37988
 acid proteinase light chain - slime mold (Physarum polycephalum) (fragment)
 C:Species: Physarum polycephalum
 C:Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 30-Sep-1993
 C:Accession: B37988
 R:Murakami-Murofushi, K.; Takahashi, T.; Minowa, Y.; Iino, S.; Takeuchi, T.; Kitagaki-og
 J. Biol. Chem. 265, 19898-19903, 1990
 A:Title: Purification and characterization of a novel intracellular acid proteinase from
 A:Reference number: A37988; MUID:91060608; PMID:2246266
 C:Accession: B37988
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-5 <MDR>

Query Match 33.3%; Score 11; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PI 4
 II
 Db 4 PI 5

RESULT 12

JS0319
 subesophageal ganglion pentapeptide - house cricket
 C:Species: Acheta domestica (house cricket)
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
 C:Accession: JS0319
 R:Wicker, C.; Wicker, C.
 Comp. Biochem. Physiol. C 88, 185-187, 1987
 A:Title: Isolation and structure of a peptide isolated from the subesophageal gangli
 A:Reference number: JS0319
 A:Accession: JS0319
 A:Molecule type: protein
 A:Residues: 1-5 <MIC>

Query Match 33.3%; Score 11; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 AVP 3
 II
 Db 2 AAP 4

RESULT 13

A61049
 halo-toxin - Pseudomonas syringae pv. mori
 C:Species: Pseudomonas syringae pv. mori
 A:Note: host mulberry tree
 C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 21-Jan-1997
 C:Accession: A61049
 R:Kajimoto, T.; Yokozaki, K.; Yahiro, K.; Umeda, T.; Shoji, S.; Kubota, Y.; Shibata,
 Chem. Lett. 00, 679-680, 1989
 A:Title: Structure of halo-toxin produced by phytopathogenic bacterium, Pseudomonas s
 A:Reference number: A61049
 A:Accession: A61049
 A:Molecule type: protein
 A:Residues: 1-6 <KAJ>
 A:Note: sequence confirmed by synthesis
 C:Comment: This toxin is one of the etiological agents of halo bright disease in mulb
 C:Keywords: toxin

Query Match 33.3%; Score 11; DB 2; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 PI 4
 II
 Db 5 PI 6

RESULT 14

PQ0008
 angiotensin-converting enzyme inhibitor (FLP-1) - common fig
 N:Alternate names: ficus latex peptide 1
 C:Species: Ficus carica (common fig)
 C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 08-Dec-1995
 C:Accession: PQ0008
 R:Maruyama, S.; Miyoshi, S.; Tanaka, H.
 Agric. Biol. Chem. 53, 2763-2767, 1989
 A:Title: Angiotensin I-converting enzyme inhibitors derived from Ficus carica.
 A:Reference number: PQ0008
 A:Accession: PQ0008
 A:Molecule type: protein

A:Residues: 1-6 <MAR>
A:Experimental source: latex
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 33.3%; Score 11; DB 2; Length 6;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PI 4
II
DB 4 PI 5

RESULT 15

B60110
repetitive protein antigen 61 - Trypanosoma cruzi (fragment)
C:Species: Trypanosoma cruzi
C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 18-Jun-1993
C:Accession: B60110
R:Hof, D.F.; Kim, K.S.; Otsu, K.; Moser, D.R.; Yost, W.J.; Blumin, J.H.; Donelson, J.E.
Infect. Immun. 57, 1959-1967, 1989
A:Title: Trypanosoma cruzi expresses diverse repetitive protein antigens.
A:Reference number: A60110; MUID:89277508; PMID:2659529
A:Accession: B60110
A>Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-6 <HOF>
A>Note: this is an example of a five residue tandem repeat from this protein; the actual
C:Keywords: tandem repeat

Query Match 33.3%; Score 11; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVP 3
II
DB 1 AAP 3

Search completed: September 13, 2003, 20:44:25
Job time : 40 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model:

Run on: September 13, 2003, 20:41:40 ; Search time 22 Seconds
(without alignments)
14.963 Million cell updates/sec

Title: US-09-939-293a-19_COPY_56_62
Perfect score: 33
Sequence: 1 AVPIAOK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 88

Minimum DB seq length: 0
Maximum DB seq length: 7

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	15	45.5	6 1 E101_LITRU	P82096 littoria rub
2	13	39.4	7 1 CARP_MYTED	P10420 mytilus edu
3	13	39.4	7 1 MNP1_LEPDE	P42884 lepidotars
4	12	36.4	6 1 OVM_LEPDE	P42885 lepidotars
5	11	33.3	5 1 SUGA_ACHDO	P19991 acheta dome
6	11	33.3	7 1 TPFY_PACDA	P83455 pachymedusa
7	10	30.3	5 1 BPP7_BOTIN	P30425 bothrops in
8	10	30.3	7 1 ALI3_CARMA	P81806 carcinus ma
9	10	30.3	7 1 ALI4_CARMA	P81807 carcinus ma
10	10	30.3	7 1 ALI5_CARMA	P81808 carcinus ma
11	10	30.3	7 1 TVS1_LITRU	P82065 littoria rub
12	9	27.3	6 1 VP19_HSVIK	P23210 herpes simp
13	8	24.2	5 1 E103_LITRU	P82099 littoria rub
14	8	24.2	5 1 PRCT_PERAM	P01373 periplaneta
15	8	24.2	6 1 CIP1_MYTED	P13736 mytilus edu
16	8	24.2	6 1 CIP2_MYTED	P13737 mytilus edu
17	8	24.2	6 1 TRP1_PSEPU	P36414 pseudomonas
18	8	24.2	7 1 E105_LITRU	P82101 littoria rub
19	8	24.2	7 1 UN06_PINPS	P81675 pinus pinas
20	7	21.2	3 1 THYL_PIG	P01151 sus scrofa
21	7	21.2	4 1 DCM1_PSECH	P19916 pseudomonas
22	7	21.2	4 1 RM01_YEAST	P36515 saccharomyc
23	7	21.2	4 1 TUFT_HUMAN	P01588 homo sapien
24	7	21.2	5 1 PAP2_PARMA	P81664 pardachirus
25	7	21.2	6 1 TMOF_SARBU	P41495 sarcophaga
26	7	21.2	7 1 CHOX_AICSP	P16101 alcaligenes
27	7	21.2	7 1 CIA_ENTFA	P11932 enterococcu
28	7	21.2	7 1 FAR1_HELTI	P41871 hellisoma tr
29	7	21.2	7 1 FAR4_PANRE	P41875 panagrellus
30	7	21.2	7 1 FAR6_CALIVO	P41866 calliphora
31	7	21.2	7 1 GFRP_MOUSE	P99025 mus musculu
32	7	21.2	7 1 LANC_CARUI	P36660 carobacter
33	7	21.2	7 1 UF04_MOUSE	P38642 mus musculu

34	6	18.2	4 1 DCM5_PSECH	P19918 pseudomonas
35	6	18.2	6 1 UN06_CLOPA	P81351 clostridium
36	6	18.2	7 1 UF03_MOUSE	P38641 mus musculu
37	6	18.2	7 1 UH11_RAF	P56576 ratus norv
38	5	15.2	3 1 GRMK_HUMAN	P01157 homo sapien
39	5	15.2	3 1 LUXE_VIBFI	P24272 vibrio fisc
40	5	15.2	4 1 FFRK_ANTFL	P58705 anthopleura
41	5	15.2	5 1 B10B_CITFR	P12997 citrobacter
42	5	15.2	5 1 E104_LITRU	P82100 littoria rub
43	5	15.2	5 1 PSK_DAUCA	P58261 daucus caro
44	5	15.2	5 1 TRM3_ECOLI	P13973 escherichia
45	5	15.2	5 1 UF01_MOUSE	P38639 mus musculu

ALIGNMENTS

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RESULT 1
E101_LITRU          STANDARD;          PRT;          6 AA.
ID E101_LITRU
AC P82096;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electric 1.
OS Littoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodytidae; Littoria.
OX NCBI_Taxid=104695;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RA Weinltz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
RT Littori electrica. Comparison with the skin peptides from Littoria
RT rubella."
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
KW Amphibian defense peptide; Amidation.
FT MOD_RES 6
FT SEQUENCE 6 AA: 792 MW: 6683704772C9A000 CRC64;
SQ
Query Match 45.5%; Score 15; DB 1; Length 6;
Best local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 2 VPI 4
Db 2 VPI 4
RESULT 2
CARP_MYTED          STANDARD;          PRT;          7 AA.
ID CARP_MYTED
AC P10420;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Catch-relaxing peptide (CARP).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
OC Mytiloidea; Mytilidae; Mytilus.
OX NCBI_Taxid=6550;
RN [1]
RP SEQUENCE.
RX MEDLINE=88052022; PubMed=3676797;
RA Hirata T., Kubota I., Takabatake I., Kawahara A., Shimamoto N.,
RA Numeoka Y.;
RT "Catch-relaxing peptide isolated from Mytilus pedal ganglia."
RL Brain Res. 422:374-376(1987).
-1- FUNCTION: THIS PEPTIDE EXHIBITS BOTH POTENTIATING (CONTRACTION)

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CC AND INHIBITORY (RELAXATION) EFFECTS ON THE ANTERIOR BYSSUS
CC RERACTOR MUSCLE.
DR PIR; A29342; ECMOCR.
KW Hormone; Amidation.
FT MOD.RES
SQ SEQUENCE 7 AA; 831 MW; 6734072687669DB0 CRC64;
AMIDATION.
Query Match 39.4%; Score 13; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. NO. 1.3e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
OY 1 AVPI 4
1:1:
Db 1 AMPM 4
RESULT 3
NMPI_LEPDE STANDARD; PRT; 7 AA.
AC P42984;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE Myotrophic neuropeptide 1 (led-MNP-1).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Physophaga; Chrysomelidae; Chrysomelidae; Chrysomelinae;
OC Chrysomelini; Leptinotarsa.
OX NCBI_TaxId=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Head;
RX MEDLINE=95380343; PubMed=7651886;
RA Spitaels K., Vankeerberghen A., Schoofs L., Torrekens S.,
RA Grauwels L., Van Leuven F., de loof A.;
RT "Identification, characterization, and immunological localization of
RT a novel myotrophic neuropeptide in the Colorado potato beetle,
RT Leptinotarsa decemlineata.";
RL Peptides 16:365-374(1995).
CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
KW Neuropeptide; Amidation.
KW MOD.RES
SQ SEQUENCE 7 AA; 705 MW; 6DD73768745B5DB0 CRC64;
Query Match 39.4%; Score 13; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. NO. 1.3e+05;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 3 PLA 5
1:1:
Db 5 PLA 7
RESULT 4
OVM_LEPDE STANDARD; PRT; 6 AA.
ID OVM_LEPDE
AC P42985;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 01-NOV-1995 (Rel. 32, Last annotation update)
DE Oviductal motility stimulating peptide (led-OVM).
OS Leptinotarsa decemlineata (Colorado potato beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
OC Physophaga; Chrysomelidae; Chrysomelidae; Chrysomelinae;
OC Chrysomelini; Leptinotarsa.
OX NCBI_TaxId=7539;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Head;
RX MEDLINE=91271080; PubMed=2052497;
RT

RA Spitaels K., Schoofs L., Grauwels L., Smet H., van Damme J.,
RA Proost P., Torrekens S., de loof A.;
RT "Isolation, identification and synthesis of novel oviductal motility
RT stimulating head peptide in the Colorado potato beetle, Leptinotarsa
RT decemlineata.";
RL Peptides 12:31-36(1991).
CC -1- FUNCTION: MYOTROPIC PEPTIDE. STIMULATES THE CONTRACTIONS OF THE
CC OVIDUCT.
KW Neuropeptide; Amidation.
KW MOD.RES
SQ SEQUENCE 6 AA; 720 MW; 6B07632B5DD03000 CRC64;
Query Match 36.4%; Score 12; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. NO. 1.3e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 4 IAOK 7
1:1:
Db 1 IAYK 4
RESULT 5
SIGA_ACHDO STANDARD; PRT; 5 AA.
ID SIGA_ACHDO
AC P1991;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE 01-OCT-1996 (Rel. 34, Last annotation update)
DE Suboesophageal ganglion pentapeptide.
OS Acheta domesticus (House cricket).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Orthoptera; Ensifera; Gryllidae; Gryllinae;
OC Acheta.
OX NCBI_TaxId=6997;
RN [1]
RP SEQUENCE.
RA Wicker C., Wicker C.;
RT "Isolation and structure of a peptide isolated from the
RT suboesophageal ganglion of Acheta domesticus (orthoptera).";
RL Comp. Biochem. Physiol. 88C:185-187(1987).
CC -1- SUBCELLULAR LOCATION: MAIN PEPTIDE FROM THE SUBESOPHAGEAL
CC GANGLIA.
DR PIR: J50319; J50319.
SQ SEQUENCE 5 AA; 476 MW; 69D76DDDB00000 CRC64;
Query Match 33.3%; Score 11; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. NO. 1.3e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
OY 1 AVP 3
1:1:
Db 2 AAP 4
RESULT 6
TPFY_PACDA STANDARD; PRT; 7 AA.
ID TPFY_PACDA
AC P83455;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tryptophyllin-1 (Pdt-1).
OS Pachymedusa dactyolor (Giant Mexican leaf frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Phyllomedusinae; Pachymedusa.
OX NCBI_TaxId=75988;
RN [1]
RP SEQUENCE, MASS SPECTROMETRY, HYDROXYLATION OF PRO-3, AND AMIDATION OF
RP PRO-7.
RC TISSUE-Skin secretion;
RA Chen T.B., Orr D.F., Shaw C.;
RX "Pachymedusa dactyolor tryptophyllin-1 (Pdt-1): structural

```

RT Characterization, pharmacological activity and cloning of precursor
RT CNA.
RL Submitted (SEP-2002) to the SWISS-PROT data bank.
CC -1- FUNCTION: Myosin. Has selective relaxing activity on vascular
CC smooth muscle.
CC -1- SURCELLULAR LOCATOR: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
CC -1- MASS SPECTROMETRY: MW=809.2; METHOD=MALDI.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0045986; P:negative regulation of smooth muscle contra. . .; NAS.
KW Amphibian defense peptide; Amidation; Hydroxylation.
FT MOD_RES 3 3 AMIDATION; HYDROXYLATION.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA: 794 MW: 7772D37DC7776350 CRC64;

Query Match 33.3%; Score 11; DB 1; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VP 3
DB 6 VP 7

RESULT 7
BPP7_BOTIN STANDARD; PRT; 5 AA.
ID BPP7_BOTIN
AC P30425;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide S5,2 (5A) (Angiotensin-converting
DE enzyme inhibitor).
OS Bothrops insularis (Island jararaca) (Quelama jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8723;
RN [1]
RP SEQUENCE.
RC TISSUE-Venom;
RX MEDLINE=90351557; Pubmed=2386615;
RA Cintra A.C.O., Vieira C.A., Giglio J.R.;
RT "Primary structure and biological activity of bradykinin potentiating
RT peptides from Bothrops insularis snake venom."
RL J. Protein Chem. 9:221-227(1990).
CC -1- FUNCTION: This peptide both inhibits the activity of the
CC angiotensin-converting enzyme and enhances the action of
CC bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR; G37196; G37196.
KW Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 5 AA: 629 MW: 776DC37326B00000 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 OK 7
DB 1 OK 2

RESULT 8
ALL3_CARMA STANDARD; PRT; 7 AA.
ID ALL3_CARMA
AC P81806;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 3. (Common shore crab) (Green crab).
OS Carcinus maenas (Common shore crab) (Green crab).

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OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and thoracic ganglion;
RX MEDLINE=98121193; Pubmed=9461295;
RA Dve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thore A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Multigene family.
SQ SEQUENCE 7 AA: 796 MW: 672879CDBC8476B70 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PIA 5
DB 2 PIA 4

RESULT 9
ALL4_CARMA STANDARD; PRT; 7 AA.
ID ALL4_CARMA
AC P81807;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 4.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Portunoidae; Portunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and thoracic ganglion;
RX MEDLINE=98121193; Pubmed=9461295;
RA Dve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
RA Thore A.;
RT "Isolation and identification of multiple neuropeptides of the
RT allatostatin superfamily in the shore crab Carcinus maenas."
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KW Neuropeptide; Multigene family.
SQ SEQUENCE 7 AA: 782 MW: 672879CDBC8476AC0 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PIA 5
DB 2 PIA 4

RESULT 10
ALL5_CARMA STANDARD; PRT; 7 AA.
ID ALL5_CARMA
AC P81808;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Carcinustatin 5.
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;

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OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Brachyura;
OC Eubrachyura; Fortunoidae; Fortunidae; Carcinus.
OX NCBI_TaxID=6759;
RN [1]
RP SEQUENCE.
RC TISSUE=Cerebral ganglion, and Thoracic ganglion;
RX MEDLINE=98421193; PubMed=9461295;
RA Duve H., Johnsen A.H., Maestro J.-L., Scott A.G., Jaros P.P.,
Thorp A.;
RT "Isolation and identification of multiple neuropeptides of the
allatostatin superfamily in the shore crab *Carcinus maenas*.";
RL Eur. J. Biochem. 250:727-734(1997).
CC -1- FUNCTION: MAY ACT AS A NEUROTRANSMITTER OR NEUROMODULATOR.
CC -1- SIMILARITY: BELONGS TO THE ALLATOSTATIN FAMILY.
KM Neuropeptide; Amidation; Multigene family.
FT MOD_RES 7
SQ SEQUENCE 7 AA; 781 MW; 672879CDBA76420 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.3e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 P1A 5
DB 2 PYA 4

RESULT 11
TY51_LITRU STANDARD; PRT; 7 AA.
ID TY51_LITRU
AC P82065;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Trypophyllin 5.1.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE-Skin secretion;
RA Steinbörner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,
Tyler M.J., Wallace J.C.;
RT "The structure of new peptides from the Australian red tree frog
Litoria rubella. The skin peptide profile as a probe for the study
of evolutionary trends of amphibians.";
RL Aust. J. Chem. 49:955-963(1996).
CC -1- FUNCTION: May act as a neuromodulator or neurotransmitter.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -1- MASS SPECTROMETRY: MW=965; METHOD=FAH.
KM Amphibian defense peptide; Amidation; Neuropeptide;
KM Pyroglutamate carboxylic acid.
FT MOD_RES 1
FT MOD_RES 7
FT MOD_RES 1
SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;

Query Match 30.3%; Score 10; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 VP 3
DB 2 IP 3

RESULT 12
VP19_HSV1K STANDARD; PRT; 6 AA.
ID VP19_HSV1K
AC P23210;
DT 01-NOV-1991 (Rel. 20, Created)

DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-DEC-1992 (Rel. 24, Last annotation update)
DE Capsid assembly and DNA maturation protein (Virion protein UL38)
DE (Capsid protein VP19C) (Fragment).
GN UL38.
OS Herpes simplex virus (type 1 / strain KOS).
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirus.
OX NCBI_TaxID=10306;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91101287; PubMed=1846198;
RA Flanagan W.M., Papavasiliou A.G., Rice M., Hecht L.B.,
Silverstein S., Wagner E.K.;
RT "Analysis of the herpes simplex virus type 1 promoter controlling the
expression of UL38, a true late gene involved in capsid assembly.";
RL J. Virol. 65:769-786(1991).
CC -1- FUNCTION: COMPONENT OF THE BASAL LAYER IN WHICH THE CAPSIDS ARE
EMBEDDED. BINDS OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
CC -1- SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP19C.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M57646; AAA45830.1; -;
KM Capsid assembly; Coat protein; DNA-binding.
FT NON_TER 6
FT SEQUENCE 6 AA; 703 MW; 67376451A336F000 CRC64;

Query Match 27.3%; Score 9; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 P1A 4
DB 5 PL 6

RESULT 13
EI03_LITRU STANDARD; PRT; 5 AA.
ID EI03_LITRU
AC P82099;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Electrin 3.
OS Litoria rubella (Desert tree frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;
OC Pelodyadinae; Litoria.
OX NCBI_TaxID=104895;
RN [1]
RP SEQUENCE.
RC TISSUE-Skin secretion;
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;
RT "Peptides from the skin glands of the Australian buzzing tree frog
Litoria rubella. Comparison with the skin peptides from Litoria
rubella.";
RL Aust. J. Chem. 52:639-645(1999).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Skin.
KM Amphibian defense peptide; Amidation.
FT MOD_RES 5
FT MOD_RES 5
FT MOD_RES 5
SQ SEQUENCE 5 AA; 630 MW; 668761P2C9A00000 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 PI 4
1:
Db 4 PM 5

RESULT 14

PROCT_PERAM STANDARD; PRT; 5 AA.
ID PROCT_PERAM STANDARD; PRT; 5 AA.
AC P1373;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE Proctolin.
OS Periplaneta americana (American cockroach),
OS Limulus polyphemus (Atlantic horseshoe crab), and
OS Carcinus maenas (Common shore crab) (Green crab).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blattodea;
OC Blattidae; Periplaneta.
OX NCBI_TaxID=6978, 6850, 6759;
RN [1]
RP SEQUENCE.
RC SPECIES-P. americana;
RX MEDLINE=76074708; PubMed=576;
RA Starratt A.N., Brown B.E.;
RT "Structure of the pentapeptide proctolin, a proposed neurotransmitter
in insects.";
RL Life Sci. 17:1253-1256(1975).
RN [2]
RP BIOLOGICAL SOURCE.
RC SPECIES-L. polyphemus;
RX MEDLINE=81225865; PubMed=6113690;
RA O'Shea M., Adams M.E.;
RT "Pentapeptide (proctolin) associated with an identified neuron.";
RL Science 213:567-569(1981).
RN [3]
RP SEQUENCE.
RC SPECIES-L. polyphemus;
RX MEDLINE=90287800; PubMed=2356151;
RA Groomer J.R., Tillinphast E.K., Townley M.A., Vetrovs A.,
RA Watson W.H. III, Hunt D.F., Griffin P.R., Alexander J.E.,
RA Shabanowitz J.;
RT "Identification of proctolin in the central nervous system of the
horseshoe crab, Limulus polyphemus.";
RL Peptides 11:205-211(1990).
RN [4]
RP SEQUENCE.
RC SPECIES-C. maenas;
RX MEDLINE=86232789; PubMed=2872661;
RA Stangier J., Dirksen H., Keller R.;
RT "Identification and immunocytochemical localization of proctolin in
pericardial organs of the shore crab, Carcinus maenas.";
RL Peptides 7:67-72(1986).
CC -1- FUNCTION: STIMULATES CARDIAC OUTPUT AND HINDGUT MOTILITY,
MODULATES VISCERAL AND SKELETAL MUSCLE IN MANY ARTHROPODS.
CC -1- TISSUE SPECIFICITY: FOUND IN THE LATERAL WHITE NEURONS AND IN
THE CRAB PERICARDIAL ORGANS.
CC PIR: A01644; HOROA.
DR PIR: A60411; A60411.
KW Neuropeptide.
SQ SEQUENCE 5 AA: 649 MW: 718767384600000 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 5;
Best Local Similarity 50.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 VP 3
1:
Db 3 LP 4

RESULT 15

CIP1_MYTED
ID CIP1_MYTED STANDARD; PRT; 6 AA.
AC P13736;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Contraction-inhibiting peptide I (MIP I).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytilloidea;
OC Mytilloidea; Mytilidae; Mytilus.
OX NCBI_TaxID=6550;
RN [1]
RP SEQUENCE.
RC TISSUE-Pedal ganglion;
RX MEDLINE=88240357; PubMed=337776;
RA Hirata T., Kubota I., Iwasawa N., Takahatake I., Ikeda T., Muneoka Y.;
RT "Structures and actions of Mytilus inhibitory peptides.";
RL Biochem. Biophys. Res. Commun. 152:1376-1382(1988).
CC -1- FUNCTION: INHIBITORY ACTION ON CONTRACTIONS IN SEVERAL MOLLUSCAN
MUSCLES.
CC -1- SIMILARITY: TO MIP II.
DR PIR: A27696; A27696.
KW hormone; Amidation.
FT MOD_RES 6
SQ SEQUENCE 6 AA: 637 MW: 72096877581000 CRC64;

Query Match 24.2%; Score 8; DB 1; Length 6;
Best Local Similarity 50.0%; Pred. No. 1.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 PI 4
1:
Db 3 PM 4

Search completed: September 13, 2003, 20:42:13
Job time : 24 secs

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OM protein - protein search, using sw model

Run on: September 13, 2003, 20:41:40 ; Search time 93 Seconds
(without alignments)
19.423 Million cell updates/sec

Title:	US-09-939-293A-19_COPY_56_62
Perfect score:	32

Perfect score: 33
Sequence: 1 AVPIAQK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 67

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Minimum DB seq length: 0
Maximum DB seq length: 7
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```
Post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :
SPREMBL_23:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp rodent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp.bacteriap:*
17: sp.archaeap:*
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SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	13	39.4	7	13	Q42564	Q42564 fungi rubrip
2	11	33.3	7	2	O50556	O50556 actinobacil
3	11	33.3	7	4	Q8NHM7	Q8NHM7 homo saplen
4	11	33.3	7	15	Q07624	Q07624 rous sarcos
5	10	30.3	5	10	Q99007	Q99007 hordium vulu
6	10	30.3	5	13	P83308	P83308 gallus gaus
7	10	30.3	7	6	Q28742	Q28742 oycetolaqus
8	10	30.3	7	10	P93233	P93233 lycopersicc
9	8	24.2	7	2	Q47477	Q47477 escherichia
10	8	24.2	7	2	P72081	P72081 nocardia la
11	8	24.2	7	2	O54248	O54248 streptomyce
12	8	24.2	7	8	O95945	O95945 saccharomyc
13	8	24.2	7	11	O63668	O63668 rattus norv
14	8	24.2	7	12	O66113	O66113 cherry lea
15	7	21.2	6	10	P82161	P82161 splinacia ol
16	7	21.2	6	10	P82162	P82162 splinacia ol

17	7	p92214	p92214 amblyoprum
18	7	p92393	p92393 hordeum vul
19	7	p92403	p92403 lophopyrum
20	7	p92427	p92427 peridictyon
21	7	p92430	p92430 aegilops ta
22	7	p92221	p92221 bromus iner
23	7	p92425	p92425 pseudoroegn
24	7	p92381	p92381 hordeum bra
25	7	p92387	p92387 henrardia p
26	7	p92210	p92210 agropyron c
27	7	p92440	p92440 thlropyrum
28	7	p92218	p92218 australopyr
29	7	p92390	p92390 heteranthel
30	7	p92372	p92372 haynaldia v
31	7	p92442	p92442 taeniatheeru
32	7	p92226	p92226 criithopsis
33	7	p92365	p92365 taraxacum (
34	7	p92385	p92385 hordeum mar
35	7	p92421	p92421 psathyrosta
36	7	p92421	p92421 psathyrosta
37	7	p92421	p92421 psathyrosta
38	7	p92421	p92421 psathyrosta
39	7	p92421	p92421 psathyrosta
40	7	p92421	p92421 psathyrosta
41	7	p92421	p92421 psathyrosta
42	7	p92421	p92421 psathyrosta
43	7	p92421	p92421 psathyrosta
44	7	p92421	p92421 psathyrosta
45	7	p92421	p92421 psathyrosta

ALIGNMENTS

RESULT 1	042564	PRELIMINARY:	PRT:	7 AA.
ID	042564			
AC	042564:			
DT	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)			
DE	Truncated voltage-gated sodium channel alpha subunit (Fragment).			
GN	SCN8A.			
OS	Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;			
OC	Acanthomorpha; Acanthopterygii; Percomorphs; Tetraodontiformes;			
OC	Tetraodontidae; Tetraodontidae; Takifugu.			
OX	NCBI_Taxid=31033;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=97442476; PubMed=9295353;			
RX	Plummer N.W., McBurney M.W., Meisler M.H.;			
RT	"Alternative splicing of the sodium channel SCN8A predicts a truncated			
RT	two-domain protein in fetal brain and non-neuronal cells."			
RL	J. Biol. Chem. 272:24008-24015(1997).			
DR	EMBL; U97673; AAB80916.1; -.			
KW	Ionic channel.			
FT	NON TER			
SO	SEQUENCE 7 AA: 730 MW: 75B72EA2C73772A0 CRC64:			
Query Match		39.4%;	Score 13;	DB 13; Length 7;
Best Local Similarity		66.7%;	Pred. NO. 8.3e+05;	
Matches	2; Conservative	1;	Mismatches	0; Indels
				0; Gaps
QY	2 VPI 4			
	11:			
Db	1 VPL 3			
RESULT 2				
ID	050556	PRELIMINARY:	PRT:	7 AA.

AC 050556;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE g1ya (Fragment).
GN GLYA.
OS Actinobacillus actinomycetemcomitans (Haemophilus
OC actinomycetemcomitans).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Actinobacillus.
OX NCBI_TaxID=714;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 33384;
RX MEDLINE=96355846; PubMed=8751884;
RA Kolodirbeiz D., Spliznagel J. Jr., Wang B., Phillips L.H., Jacobs C.,
RA Kralj B.;
RT "cis Elements and trans factors are both important in strain-specific
RT regulation of the leukotoxin gene in Actinobacillus
RT actinomycetemcomitans."
RL Infect Immun. 64:3451-3460(1996).
DR EMBL; 051862; AAB8721.1; -.
FT NON_TER
SQ SEQUENCE 7 AA; 832 MW; 6DCB42D767340420 CRC64;

Query Match 33.3%; Score 11; DB 2; Length 7;
Best Local Similarity 33.3%; Pred. No. 8.3e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 VPI 4
DB 3 LPV 5

RESULT 3
OBNHH7
ID OBNHH7; PRELIMINARY; PRT; 7 AA.
AC OBNHH7;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Minl-cistron.
GN NHE3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Malakooti J., Ramaswamy K.;
RT "Molecular cloning and characterization of the human Na+/H+ exchanger
RT NHE-3 gene promoter region."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF282824; AAM53436.1; -.
SQ SEQUENCE 7 AA; 842 MW; 74072DC772DA06F0 CRC64;

Query Match 33.3%; Score 11; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 VP 3
DB 3 VP 4

RESULT 4
007624
ID 007624; PRELIMINARY; PRT; 7 AA.
AC 007624;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE DORF1.

OS Rous sarcoma virus (strain Prague C).
OC Viruses; Retroid viruses; Retroviridae; Alpharetrovirus.
OX NCBI_TaxID=11888;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93010967; PubMed=1327749;
RA Donze O., Spahr P.F.;
RT "Role of the open reading frames of Rous sarcoma virus leader RNA in
RT translation and genome packaging."
RL EMBO J. 11:3747-3757(1992).
DR EMBL; X67587; CAA47862.1; -.
SQ SEQUENCE 7 AA; 672 MW; 776045A7687DD6F0 CRC64;

Query Match 33.3%; Score 11; DB 15; Length 7;
Best Local Similarity 33.3%; Pred. No. 8.3e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 AVP 3
DB 5 STP 7

RESULT 5
099007
ID 099007; PRELIMINARY; PRT; 5 AA.
AC 099007;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Alpha amylase (Fragment).
GN AMY GENE.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OX Trilicaceae; Hordeum.
OX NCBI_TaxID=4513;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91329704; PubMed=1831055;
RA Jacobsen J.V., Close T.J.;
RT "Control of transient expression of chimaeric genes by gibberellic
RT acid and abscisic acid in protoplasts prepared from mature barley
RT aleurone layers."
RL Plant Mol Biol. 16:713-721(1991).
DR EMBL; X54643; CAA38455.1; -.
FT NON_TER
SQ SEQUENCE 5 AA; 600 MW; 61E3344DD6F00000 CRC64;

Query Match 30.3%; Score 10; DB 10; Length 5;
Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 IAKK 7
DB 1 MANK 4

RESULT 6
P83308
ID P83308; PRELIMINARY; PRT; 5 AA.
AC P83308;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE FMRFamide-like neuropeptide (LPLNF-amide).
OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OX Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Brain;

```

RX PubMed-6137771;
RA Dockray G.J., Reeve J.R. Jr., Shively J., Gayton R.J., Barnard C.S.;
RT "A novel active pentapeptide from chicken brain identified by
RT antibodies to FMRFamide.";
RL Nature 305:328-330(1983).
CC -1- FUNCTION: MAY FUNCTION AS A NEUROTRANSMITTER OR MODULATOR.
CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KW Neuropeptide.
SQ SEQUENCE 5 AA; 645 MW; 69D4073767400000 CRC64;

Query Match          30.3%; Score 10; DB 13; Length 5;
Best Local Similarity 33.3%; Pred. No. 8.3e+05;
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VPI 4
   1:
DB 1 LPL 3

RESULT 7
ID 028742 PRELIMINARY; PRT; 7 AA.
AC 028742;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE Alpha-myosin heavy chain (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-84221901; PubMed-6328491;
RA Friedman D.J., Umeda P.K., Sinha A.M., Hsu H.-J., Jokovic S.,
RA Rabinowitz M.;
RT "Characterization of genomic clones specifying rabbit alpha- and beta-
RT ventricular myosin heavy chains.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:3044-3048(1984).
DR EMBL; K01698; AAA31415.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 916 MW; 6B1B1A1E69326B0 CRC64;

Query Match          30.3%; Score 10; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 OK 7
   1:
DB 1 OK 2

RESULT 8
ID P93233 PRELIMINARY; PRT; 7 AA.
AC P93233;
DT 01-MAY-1997 (TREMblrel. 03, Created)
DT 01-MAY-1997 (TREMblrel. 03, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase (DC 4.4.1.14)
DE (Fragment).
GN LE-ACS1B.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97351561; PubMed-9207843;
RA Oetliker J.H., Olson D.C., Shu O.Y., Yang S.F.;
RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate

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RT synthase genes by elicitor in suspension cultures of tomato
RT (Lycopersicon esculentum).";
RL Plant Mol. Biol. 34:275-286(1997).
DR EMBL; U75692; AAC49682.1; -.
KW lyase.
FT NON_TER 1
SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;

Query Match          30.3%; Score 10; DB 10; Length 7;
Best Local Similarity 25.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 PIAQ 6
   1:
DB 3 PLVR 6

RESULT 9
ID 047477 PRELIMINARY; PRT; 7 AA.
AC 047477;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-MAY-1999 (TREMblrel. 10, last sequence update)
DT 01-MAY-1999 (TREMblrel. 10, last annotation update)
DE Tpi protein (Fragment).
GN TPI.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE OF 7-7 FROM N.A.
RX MEDLINE-85203917; PubMed-3158524;
RA Hellings H.W., Evans P.R.;
RT "Nucleotide sequence and high-level expression of the major
RT Escherichia coli phosphofructokinase.";
RL Eur. J. Biochem. 149:363-373(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA Evans P.;
RT Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
DR EMBL; X02519; CAA26359.1; -.
FT NON_TER 1
SQ SEQUENCE 7 AA; 773 MW; 7416D33DDDB1DB0 CRC64;

Query Match          24.2%; Score 8; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 8.3e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 AQR 7
   1:
DB 3 AAK 5

RESULT 10
ID P72081 PRELIMINARY; PRT; 7 AA.
AC P72081;
DT 01-FEB-1997 (TREMblrel. 02, Created)
DT 01-FEB-1997 (TREMblrel. 02, last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)
DE 3'-methylcephem hydroxylase (Fragment).
GN CEF3.
OS Nocardia lactamdurans.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Pseudonocardiaceae; Pseudonocardiaceae; Amycolatopsis.
OX NCBI_TaxID=1913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-96009872; PubMed-7557411;
RA Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,
RA Liras P.;
RT "Characterization of the cmh genes of Nocardia lactamdurans and

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RT Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem
 RT O-carbamoyltransferase for cephamycin biosynthesis."
 RL Gene 162:21-27(1995).
 DR EMBL; 221682; CAA79797.1; -.
 FT NON_TER
 SQ SEQUENCE 7 AA; 746 MW; 75A1B2CDD1E681C0 CRC64;

Query Match 24.2%; Score 8; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AV 2
 II
 DB 4 AV 5

RESULT 11
 ID 054248 PRELIMINARY; PRT; 7 AA.
 AC 054248;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE RplO protein (Fragment).
 GN RplO.
 OS Streptomyces griseus.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1911;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=N2-3-11;
 RX MEDLINE=20011291; PubMed=10542330;
 RA Poehling S., Piepersberg W., Wehmeler U.F.,
 RT "Analysis and regulation of the sec Y gene from Streptomyces griseus
 RT N2-3-11 and interaction of the secY protein with the SecA protein."
 RL Biochim. Biophys. Acta 1447:298-302(1999).
 DR EMBL; X95915; CAA65160.1; -.
 FT NON_TER
 SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;

Query Match 24.2%; Score 8; DB 2; Length 7;
 Best Local Similarity 20.0%; Pred. No. 8.3e+05;
 Matches 1; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 VP1A 6
 I : :
 DB 1 VTYTE 5

RESULT 12
 ID 095945 PRELIMINARY; PRT; 7 AA.
 AC 095945;
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Inside intron 5 (Fragment).
 OS Saccharomyces cerevisiae (Baker's yeast).
 OG Mitochondrion.
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=D273-10B;
 RX MEDLINE=81069885; PubMed=6254986;
 RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;
 RT "Assembly of the mitochondrial membrane system: Structure and
 RT nucleotide sequence of the gene coding for subunit I of yeast
 RT cytochrome oxidase."
 RL J. Biol. Chem. 255:11927-11941(1980).
 DR EMBL; V00694; CAA24066.1; -.

KW Mitochondrion.
 FT NON_TER
 SQ SEQUENCE 7 AA; 859 MW; 75B7233362CDC460 CRC64;

Query Match 24.2%; Score 8; DB 8; Length 7;
 Best Local Similarity 100.0%; Pred. No. 8.3e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 AV 2
 II
 DB 2 AV 3

RESULT 13
 ID 063668 PRELIMINARY; PRT; 7 AA.
 AC 063668;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE ORF2 protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Kidney;
 RX MEDLINE=95396550; PubMed=7667072;
 RA Mandon B., Bellanger A.C., Elalouf J.M.;
 RT "Inverse-PCR-mediated cloning of the promoter for the rat vasopressin
 RT V2 receptor gene."
 RL Plügers Arch. 430:12-18(1995).
 DR EMBL; X83264; CAA58237.1; -.
 FT NON_TER
 SQ SEQUENCE 7 AA; 703 MW; 75A767287DC6D6F0 CRC64;

Query Match 24.2%; Score 8; DB 11; Length 7;
 Best Local Similarity 50.0%; Pred. No. 8.3e+05;
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 VP 3
 I : :
 DB 5 LP 6

RESULT 14
 ID 066113 PRELIMINARY; PRT; 7 AA.
 AC 066113;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE C-terminus of the viral replicase (Fragment).
 OS Cherry leaf roll virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
 OC Nepovirus.
 OX NCBI_TaxID=12615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=walnut;
 RA Borja M.;
 RL Thesis (1992), Biología Molecular y Virología Vegetal, CIT-INIA.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=walnut;
 RX MEDLINE=96124520; PubMed=8560786;
 RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
 RT "Long, nearly identical untranslated sequences at the 3' terminal
 RT regions of the genomic RNAs of cherry leafroll virus (walnut
 RT strain)."
 RL Virus Genes 10:245-252(1995).
 DR EMBL; Z34265; CAA84019.1; -.
 FT NON_TER
 I 1

SO SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 24.2%; Score 8; DB 12; Length 7;
Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 VP 3
1
DB 5 LP 6

RESULT 15

P82181 PRELIMINARY; PRT; 6 AA.
AC P82181;
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Chloroplast 50S ribosomal protein L10 beta (fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE.
RC STRAIN-CV. ALMARO; TISSUE-Leaf;
RX MEDLINE=20435798; PubMed=10874046;
RA Yamaguchi K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
the 50 S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28466-28482(2000).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 16.5 KDA.
CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
DR InterPro: IPR001790; Ribosomal_L10.
DR Pfam: PF00466; Ribosomal_L10ub.
DR PROSITE: PS01109; RIBOSOMAL_L10; PARTIAL.
KW Ribosomal protein; Chloroplast; rRNA-binding.
FT NON_TER
SQ SEQUENCE 6 AA; 675 MW; 6321B415B05DB000 CRC64;

Query Match 21.2%; Score 7; DB 10; Length 6;
Best Local Similarity 50.0%; Pred. No. 8.3e+05;
Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 AV 2
1
DB 1 AI 2

Search completed: September 13, 2003, 20:46:08
Job time : 97 secs

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Db 2 IPVLOK 7

RESULT 2

US-08-313-127A-10
; Sequence 10, Application US/08313127A
; Patent No. 5618699

GENERAL INFORMATION:

APPLICANT: HAMAMOTO, Hiroshi
APPLICANT: SUGIYAMA, Yoshinori
APPLICANT: NAKAGAWA, No. 5618699iak1
APPLICANT: HASHIDA, Elji
APPLICANT: TSUCHIMOTO, Suguru
APPLICANT: NAKANISHI, No. 5618699iyuki
APPLICANT: MATSUNAGA, Yoji
APPLICANT: OKADA, Yoshimi
TITLE OF INVENTION: PLANT VIRUS VECTOR, PLASMID,
TITLE OF INVENTION: PROCESS FOR EXPRESSION OF
TITLE OF INVENTION: FOREIGN GENE AND PROCESS FOR
TITLE OF INVENTION: OBTAINING FOREIGN GENE PRODUCT
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: SUGHRUE, MIOM, ZINN, MACPEAK & SEARS
STREET: 2100 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
ZIP: 20037

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313.127A
FILING DATE: 30-SEPT-1994
CLASSIFICATION: 435

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PCT/JP 93/00408
FILING DATE: 31-MAR-1994
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
TELEX: 6491103

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-313-127A-10Query Match 60.6%; Score 20; DB 1; Length 7;
Best Local Similarity 57.1%; Pred. No. 2.5e+05;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 AVPIAQ 7

Db 1 AVPYQR 7

RESULT 3

US-09-492-766-8
; Sequence 8, Application US/09492766
; Patent No. 6506732

GENERAL INFORMATION:

APPLICANT: AMIOF, Jean
TITLE OF INVENTION: ENZYMATIC HYDROLYSATE OF MILK PROTEINS
FILE REFERENCE: 6013-57"US"
CURRENT APPLICATION NUMBER: US/09/492.766
CURRENT FILING DATE: 2000-01-27
EARLIER APPLICATION NUMBER: 60/117,661

; EARLIER FILING DATE: 1999-01-28

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 8

; LENGTH: 7

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Peptide from enzymatic hydrolysate of milk

US-09-492-766-8

Query Match 60.6%; Score 20; DB 4; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.5e+05;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 VPIAQ 7

Db 2 LPVPQR 7

RESULT 4

US-08-592-646A-60
; Sequence 60, Application US/08592646A
; Patent No. 5851335

GENERAL INFORMATION:

APPLICANT: JOLIVET-REYNAUD, Colette
TITLE OF INVENTION: MIMOTOPIC POLYPEPTIDES OF TOKOPLASMA
TITLE OF INVENTION: GONDII AND APPLICATIONS
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSEE: OLIVE & BERRIDGE, PLC
STREET: P.O. Box 19928
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592.646A
FILING DATE: 26-JAN-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Berridge, William P.
REGISTRATION NUMBER: 30,024
REFERENCE/DOCKET NUMBER: WPB 36923
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703 836-6400
TELEFAX: 703 836-2787

INFORMATION FOR SEQ ID NO: 60:

SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-646A-60

Query Match

54.5%; Score 18; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PIAQ 6

Db 1 PIAQ 4

RESULT 5

US-09-165-422-60

; Sequence 60, Application US/09165422
; Patent No. 6372897
; GENERAL INFORMATION:
; APPLICANT: JOLIVET-REYNAUD, Colette
; TITLE OF INVENTION: MINOTOPIC POLYPEPTIDES OF TOXOPLASMA
; REAGENTS
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: OLIVIER & BERRIDGE, PLC
; STREET: P.O. Box 19928
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/165,422
; FILING DATE: 02-Oct-1998
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Berridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 36923
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703 836-6400
; TELEFAX: 703 836-2787
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-165-422-60

Query Match 54.5%; Score 18; DB 4; Length 4;
Best Local Similarity 75.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 P1A0 6
1:11
Db 1 P1A0 4

RESULT 6
5217869-41
; Patent No. 5217869
; APPLICANT: KAVVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO: 41:
; LENGTH: 5
5217869-41

Query Match 54.5%; Score 18; DB 6; Length 5;
Best Local Similarity 60.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

5217869-90
; Patent No. 5217869
; APPLICANT: KAVVAR, LAWRENCE M.
; TITLE OF INVENTION: METHOD TO PRODUCE IMMUNODIAGNOSTIC
; REAGENTS
; NUMBER OF SEQUENCES: 121
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/255,906
; FILING DATE: 11-OCT-1988
; SEQ ID NO: 90:
; LENGTH: 5
5217869-90

Query Match 54.5%; Score 18; DB 6; Length 5;
Best Local Similarity 75.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 P1A0 6
1:11
Db 1 P1A0 4

RESULT 8
US-08-325-509-46
; Sequence 46, Application US/08325509
; Patent No. 5543308
; GENERAL INFORMATION:
; APPLICANT: MORGAN, RICHARD D.
; TITLE OF INVENTION: ISOLATED DNA ENCODING THE PseI
; TITLE OF INVENTION: RESTRICTION ENDONUCLEASE AND RELATED METHODS FOR
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: GREGORY D. WILLIAMS; NEW ENGLAND
; STREET: 32 TOZER ROAD
; CITY: BEVERLY
; STATE: MASSACHUSETTS
; COUNTRY: US
; ZIP: 01915
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,509
; FILING DATE: 18-OCT-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, GREGORY D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: NEB-104
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 927-5054
; TELEFAX: (508) 927-1705
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-325-509-46

Query Match 54.5%; Score 18; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVPI 4
1:11
Db 3 AVPI 6

RESULT 9
US-08-584-579-1
; Sequence 1, Application US/08584579
; Patent No. 5674979
; GENERAL INFORMATION:
; APPLICANT: Schramm, Wolfgang
; TITLE OF INVENTION: Agent for Inhibiting Symmetrical
; TITLE OF INVENTION: Proteins, in Particular Enzymes
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Venable, Baetjer, Howard & Civiletti
; STREET: 1201 New York Avenue N.W., Suite 1000
; City: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/584,579
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/332,447
; FILING DATE: 31-OCT-1994
; APPLICATION NUMBER: US 08/112,215
; FILING DATE: 26-AUG-1993
; APPLICATION NUMBER: US 07/976,003
; FILING DATE: 13-NOV-1992
; APPLICATION NUMBER: US 07/585,141
; FILING DATE: 07-DEC-1990
; APPLICATION NUMBER: WO PCT/EP90/00219
; FILING DATE: 09-FEB-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 39 04 040.2
; FILING DATE: 10-FEB-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Imnen, Jeffrey L.
; REGISTRATION NUMBER: 28957
; REFERENCE/DOCKET NUMBER: 18644-96040
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-962-8300
; TELEFAX: 202-962-8300
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: YES
; US-08-584-579-1

Query Match
Best Local Similarity 54.5%; Score 18; DB 1; Length 6;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AVPIA 5
1 1 1 1
DB 2 APPIA 6

RESULT 10
US-09-121-964-7
; Sequence 7, Application US/09121964
; Patent No. 6124447
; GENERAL INFORMATION:
; APPLICANT: Natoli, Shunji
; TITLE OF INVENTION: NOVEL ENZYME CATALYZING DEPHOSPHORYLATION

; FILE REFERENCE: 32290-144753
; CURRENT APPLICATION NUMBER: US/09/121,964
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Sarcophaga peregrina
US-09-121-964-7

Query Match
Best Local Similarity 54.5%; Score 18; DB 3; Length 7;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVPI 4
1 1 1 1
DB 1 AVPIV 4

RESULT 11
5496927-1
; Patent No. 5496927
; APPLICANT: KOEB, H.MICHAEL, BURKHART, JOSEPH P.; JUNG, MICHEL J.;
; GERHART, FRITZ E.; GIROUX, EUGENE L.; NEISES, BERNHARD; SCHIRLIN,
; DANIEL G.
; TITLE OF INVENTION: PEPTIDASE INHIBITORS
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,847
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 102,522
; FILING DATE: 04-AUG-1993
; APPLICATION NUMBER: 980,141
; FILING DATE: 23-NOV-1992
; APPLICATION NUMBER: 540,033
; FILING DATE: 19-JUN-1990
; APPLICATION NUMBER: 372,162
; FILING DATE: 27-JUN-1989
; APPLICATION NUMBER: 267,758
; FILING DATE: 01-NOV-1988
; APPLICATION NUMBER: 874,721
; FILING DATE: 15-JUN-1986
; APPLICATION NUMBER: 697,987
; FILING DATE: 04-FEB-1985
; SEQ ID NO: 1:
; LENGTH: 4
5496927-1

Query Match
Best Local Similarity 51.5%; Score 17; DB 6; Length 4;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVPI 4
1 1 1 1
DB 1 AVPIV 4

RESULT 12
5496927-2
; Patent No. 5496927
; APPLICANT: KOEB, H.MICHAEL, BURKHART, JOSEPH P.; JUNG, MICHEL J.;
; GERHART, FRITZ E.; GIROUX, EUGENE L.; NEISES, BERNHARD; SCHIRLIN,
; DANIEL G.
; TITLE OF INVENTION: PEPTIDASE INHIBITORS
; NUMBER OF SEQUENCES: 26
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/248,847
; FILING DATE: 25-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 102,522
; FILING DATE: 04-AUG-1993

APPLICATION NUMBER: 980,141
FILING DATE: 23-NOV-1992
APPLICATION NUMBER: 540,033
FILING DATE: 19-JUN-1990
APPLICATION NUMBER: 372,162
FILING DATE: 27-JUN-1989
APPLICATION NUMBER: 267,758
FILING DATE: 01-NOV-1988
APPLICATION NUMBER: 874,721
FILING DATE: 15-JUN-1986
APPLICATION NUMBER: 697,987
FILING DATE: 04-FEB-1985
SEQ ID NO: 2
LENGTH: 6
5496927-2

Query Match 51.5%; Score 17; DB 6; Length 6;
Best Local Similarity 50.0%; Pred. No. 2.5e+05;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 AVPI 4
1:1:
Db 1 AIPV 4

RESULT 13
US-08-618-693-96
Sequence 96, Application US/08618693
Patent No. 5723594
GENERAL INFORMATION:
APPLICANT: NEROUSA JANJIC
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY PDGF NUCLEIC
TITLE OF INVENTION: ACID LIGANDS
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/618, 693
FILING DATE: 20 MARCH 1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,783
FILING DATE: 7-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX42/CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Peptide
FEATURE:
OTHER INFORMATION: Xaa at position 5 is a
OTHER INFORMATION: modified amino acid that could not be identified.
US-08-618-693-96

Query Match 51.5%; Score 17; DB 1; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.5e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 PINAK 7
1:1:
Db 3 PIXKK 7

RESULT 14
US-08-973-124-185
Sequence 185, Application US/08973124
Patent No. 6207816
GENERAL INFORMATION:
APPLICANT: LARRY GOLD et al.
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO GROWTH
NUMBER OF SEQUENCES: 304
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,124
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08014
FILING DATE: 30-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,423
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,594
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,591
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,725
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,783
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618, 693
FILING DATE: 20-MARCH-1996
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: Peptide

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;
; FEATURE:
; OTHER INFORMATION: xaa at position 5 is a modif
; OTHER INFORMATION: that could not be identified.
US-08-973-124-185

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Query Match
Best Local Similarity 51.5%; Score 17; DB 3; Length 7;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY
3 PIAOK 7
11:1
Db
3 PIXKK 7

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RESULT 15
US-08-991-743C-96
; Sequence 96, Application US/08991743C.
; Patent No. 6229002
; GENERAL INFORMATION:
; APPLICANT: NEROJA JANJIC, LARRY GOLD
; TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR (PDGF) NUCLEIC
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSSEE: Swanson and Bratschun, L.L.C.
; STREET: 1745 Shea Center Drive, Suite 330
; CITY: Highlands Ranch
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80129
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/991,743C
; FILING DATE: 16-Dec-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/618,693
; FILING DATE: 20-MARCH-1996
; APPLICATION NUMBER: 08/479,783
; FILING DATE: 7-JUNE-1995
; APPLICATION NUMBER: 08/479,725
; FILING DATE: 7-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX66
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 268-0066
; TELEFAX: (303) 268-0065
; INFORMATION FOR SEQ ID NO: 96:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FEATURE:
; OTHER INFORMATION: xaa at position 5 is a modified amino acid
; that could not be identified.
; SEQUENCE DESCRIPTION: SEQ ID NO: 96:
US-08-991-743C-96

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Query Match
Best Local Similarity 51.5%; Score 17; DB 3; Length 7;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY
3 PIAOK 7
11:1
Db
3 PIXKK 7

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Search completed: September 13, 2003, 20:46:41
Job time: 31 secs